CYTOGENETIC AND GENETIC ANALYSES OF CERTAIN CHARACTERS IN COMMON WHEAT USING WHOLE CHROMOSOME SUBSTITUTION LINES

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CYTOGENETIC AND GENETIC ANALYSES OF CERTAIN CHARACTERS IN COMMON WHEAT USING WHOLE CHROMOSOME SUBSTITUTION LINES.

I INTRODUCTION

Genetic analyses of quantitative characters in polyploid organisms such as the hexaploid common wheat, Triticum vulgare Vill., (= Triticum aestivum L. emend Fiori et Paoletti), have only rarely been successful. The chief reason for failure is that polyploids are not very amenable to orthodox methods of genetic analyses. This is due to several factors:

(a) the duplication or even triplication of genic material,

(b) the presence of minor genes or modifiers,

(c) the difficulty or impossibility of making accurate classifications of segregants,

(d) the difficulty of determining linkages because of the large number of chromosomes.

With the isolation of plants with various chromosomal aberrations in common wheat by Sears a new method of analysis has been made possible. Using *nullisomics, **monotelosomics or ***mono-isosomics for the twenty-one chromosomes in Chinese Spring+, single chromosomes of this variety can be replaced by their homologues from the donor variety. The effect of genes on these substituted chromosomes on various quantitative and qualitative characters can be studied in a uniform genetic background of Chinese by comparing substitution lines with the normal recipient variety.

This report deals with the use of three distinct sets of Chinese substitution lines in studying the genetics of awning, earliness, height, lodging, protein content, spike density, thousand-kernel weight and yield. The first set of Chinese substitution lines comprises 19 chromosomes of Thatcher substituted for their respective homologues in Chinese; chromosome XIV and XVII lines are not included in this study. The remaining two sets are composed of Hope and Timstein chromosomes respectively. Chromosome lines XIII and XIV in both of the latter sets were not available when the study was begun.

*Nullisomic - any individual deficient for a single pair of homologous chromosomes (2n-2).

**Monotelosomic - an individual which has twenty pairs of chromosomes and a telocentric chromosome for one of the arms of either chromosome of the missing pair.

20" + telocentric

***Mono-isosomic - an individual which has twenty pairs of chromosomes and an isochromosome for one of the arms of either chromosome of the missing pair.

20" + isochromosome

+ Throughout the report Chinese Spring is contracted to Chinese.

II REVIEW OF LITERATURE

1. Cytologic Investigations of Nullisomics, Monosomics, Telocentric Chromosomes, and Isochromosomes.

A. Cytologic Investigations of Monosomic Plants

Monosomics are diploid or polyploid individuals that are deficient for an entire chromosome. The best known monosomic in diploids is the haple - IV type of Drosophila melanogaster. Apparently, because of duplication of essential genetic material, polyploids can tolerate deficiencies that would result in the death or partial development followed by death in diploid organisms who have smaller reserves of essential genetic material. Thus monosomic individuals are obtained much more frequently and readily in polyploids than in diploids.

Clausen (18) reported obtaining 20 of the 24 possible monosomics in Nicotiana tabacum (2n=48) and Clausen and Cameron (19) reported that the 24 different monosomics had been isolated. These different monosomics have been used with marked success in associating genes with chromosomes. In associating recessive genes with particular chromosomes a normal recessive line is crossed with each of the 24 monosomics. The resulting F_1 populations for the respective chromosomes are composed of both monosomic and disomic plants. In the critical F_1 family only the monosomic plants are of the recessive phenotype and all the disomic plants exhibit the dominant form of the characteristic as do all plants in non critical families. To test for the association of dominant genes with chromosomes, the dominant type is crossed to each of the 24 monosomic lines. The F_1's are selfed and F_2 populations are grown. The critical F_2 family shows no recessive segregates since nullisomics are not obtained because the 23-chromosome pollen is not viable. In non-critical F_2 families the expected number of recessive segregates

will appear. Duplicate genes for chlorophyll production in Nicotiana Tabacum have been located by Clausen and Cameron (20) using monosomic analysis.

Olmo (57) described 7 monosomic types of Nicotiana Tabacum var. purpurea which originated from progenies of interspecific hybrids or through non-conjunction of chromosomes in otherwise normal plants. He observed that monosomics were less fertile than the normal purpurea strain and he calculated that 45.6 to 83.2% of the female gametes of monosomic plants were n-1 while the transmission of n-1 male gametes of monosomic plants ranged from 0 to 7% with 2% being an approximate average.

Lammerts (44) working with Nicotiana rustica (2n = 48) studied the transmission of whole chromosome deficiencies through the eggs and pollen. The percentage of functional female n-1 gametes of monosomic plants ranged from 31 to 75%. This range in percentage of functional female n-1 gametes was due mostly to differential lagging of the univalent. In certain cases low transmission of the deficiency may be due to: (a) selective development at 4-celled stage of megasporogenesis,

(b) frequent failure of 2n-1 zygotes to complete normal seed development.

In only 3 of the 7 monosomics studied was the deficiency transmitted with an appreciable frequency through the pollen. Lammerts stated that, "viability of n-1 gametes and 2n-2 zygotes is evidence that a species is polyploid".

Greenleaf (31) studied transmission of n and n-1 female gametes in monosomic types of Nicotiana Tabacum. On the basis of cytological observations he concluded that two causes were responsible for lowered transmission of n-1 functional eggs: (a) slow rate of development of n-1 embryo sacs and (b) a higher frequency of embryo sac abortion prior

to the 8-nucleate stage. He assumed that the frequency of univalent elimination is the same in megasporogenesis as in microsporogenesis and that about 80% of all megaspores are n-1, regardless of the chromosome concerned. Frequency of functioning of n-1 embryo sacs would then depend on the relative importance of the missing chromosome in the process of embryo sac development.

Many investigations of whole chromosome deficiencies have been carried on in common wheat (T. vulgare). In most of these cases, the deficiency concerned was chromosome IX(C) which when present as a monosome causes heterozygous speltoidy as shown by Huskins (36, 37), Huskins and Spier (38), Hakansson (cited by Sears, 71) and Sears (71). Two monosomics were found by Nishiyama (56) among the progeny of a cross between two nullisomics of F_4 (T. polonicum x T. spelta) x T. spelta. Powers (62) found that two of the 32 Marquillo plants he examined were monosomic. Love (48) obtained numerous monosomic plants in 50 lines derived from crosses of 4 varieties of T. vulgare with T. durum var. Iumillo. Sears (69, 71, 76) has isolated all 21 possible monosomic types in the common wheat variety Chinese.

Nishiyama (56) who studied transmission of effective n and n-1 gametes through both the male and female in monosomics of the forementioned cross found the proportion of 20-and 21-chromosome megaspores in the ratio of 73:27, and that the ratio of 20-and 21-chromosome microspores was 11:89. Powers (62) found that 23.4 ∓ 0.24% of microspores of monosomic plants showed micronuclei. On the basis of the number of microspores showing micronuclei the expected ratio of 20:21 chromosome female gametes was determined as 74:26. Sears (69) outlined the possible methods of origin of monosomics and in a later paper (71) reported that in monosomics 75% of the functional female gametes are

deficient for the monosome regardless of the chromosome concerned. Male transmission of functional 20-chromosome gametes varies from approximately 1 to 15% depending on the chromosome. No evidence was found of any selection against n-1 gametes such as that observed by Greenleaf (31) in Nicotiana Tabacum. Regarding transmission of deficiencies by both male and female gametes, the resultsof these three workers are in close agreement.

In the studies of Powers (62) and Myers and Powers (52), the presence of micronuclei in quartets was found to be correlated with the monosomic condition. The percentage of microspores showing micronuclei in disomics of Marquillo, Marquis, Minnesota 2303, and in monosomic plants of Marquillo was 23.4± 0.24, 2.8, 0.8, and 0.8% respectively. Observations showed that genetic irregularities and meiotic instability were often associated with cytologic anomalies. Love (48) reported that the percentage of quartets exhibiting micronuclei varied with the monosomics.

B. Cytologic Investigations of Nullisomic Plants

Nullisomics are individuals deficient for one pair of chromosomes. They have been reported rarely and only in polyploid organisms.

In Nicotiana Tabacum, an allotetraploid with 24 pairs of chromosomes, all of the possible different monosomics but no nullisomics have been obtained Olmo (57), Clausen (18), Clausen and Cameron, (19). Similarly in seven different monosomics in Nicotiana rustica Lammerts (44) was unable to obtain nullisomic progenies. Since several types of 23- chromosome male gametes have proved partially functional the failure of nullisomics to appear in N. Tabacum and N. rustica is probably due primarily to inviability of nullisomic zygotes.

In common oats, Avena sativa, which is hexaploid, Huskins (35),

Smith, Huskins and Sander (80) found that homozygous B-type fatuoids (offtypes in common oats resembling Avena fatua) have only 20 pairs of chromosomes, these were obtained in the progeny of heterozygous fatuoids (20" + 1'). Philp (60, 61) isolated two additional nullisomics.

In common wheat, Triticum vulgare, nullisomics have been obtained by several investigators. Many of these deficiencies have evidently involved the same chromosome, the "C"(IX) or speltoid chromosome. Homozygous B-type speltoids (20") have been found in the progeny of monosomic "C"(IX) plants as has been shown by Huskins (36), Smith, Huskins and Sander (80) and Sears (71).

Nullisomics other than those involving chromosome "C"(IX) also have been isolated. Nullisomic dwarfs or semi-dwarfs have been obtained by Thompson (99) following a varietal cross in T. vulgare by Kihara (cited by Thompson, 99) among derivatives of T. polonicum x T. spelta and by Uchikawa (101). Love (48) found nullisomic plants and also nullisomic lines in 50 strains, in the F_5 to F_7, selected for various agronomic characters from hybrids of 4 varieties of T. vulgare x T. durum var. Iumillo. Most of the nullisomic lines were partially fertile.

The origin and characteristics of 7 nullisomics were described by Sears in 1941 at which time their possible usefulness for genetic analysis and breeding was also pointed out. Compared to normal (21") plants all the nullisomics were less vigorous and fertile, however, all were female fertile and 4 produced functional pollen. In 1944 Sears described 17 of the 21 possible nullisomics in Chinese. None were found to be completely sterile, ten or eleven were fertile as both male and female, five or six were female fertile only, and one was male fertile only. All the 21 nullisomics have now been obtained (sears, 76). Considerable progress has already been made in associating genes with chromosomes using nullisomics.

Because the A and B genome chromosomes of *Triticum vulgare* pair regularly with wheats of the emmer group (A and B genomes) a 34-chromosome hybrid of a monosomic plant of *T. vulgare* with a member of the emmer group will show at meiosis whether or not the univalent concerned is a chromosome homologous with one of emmer. The nullisomic were numbered I to XIV in the order they were obtained if the chromosome involved was homologous to a particular chromosome of the emmer or tetraploid wheats. Those nullisomics that corresponded to a particular chromosome of the C(D) genome of common wheat were numbered XV to XXI in the order in which they were obtained.

C. Cytologic Investigations of Plants with Telocentric Chromosomes and Isochromosomes

Telocentric chromosomes are aberrant chromosomes that are deficient for one whole arm and have a terminal centromere. Isochromosomes are chromosomes that are deficient for one arm but duplicated for the other. These aberrations have been observed in several plant species and certain types of anomalous behaviour have been noted where detailed studies have been carried out. Upcott (103) Koller (43) and Darlington (21) discovered that both telocentric chromosomes and isochromosomes arise through misdivision of univalents.

Rhoades (65), working with maize (*Zea mays*), found a telocentric chromosome consisting of the short arm of chromosome 5 to be unstable in somatic tissue, tending to be entirely lost or reduced in size. At pollen mitosis it occasionally gave rise to an isochromosome.

Love (47) working with the variety Dawson's Golden Chaff found 2 different off-type "mutants" each with 20 normal and 1 telocentric pair

of chromosomes. F_1's of crosses between these 2 off-types exhibited 2 heteromorphic bivalents; this indicated that the telocentrics were fragments of two different chromosomes. One of the "mutants" was white chaffed indicating that the lost arm carried the gene for red chaff color in that variety. He described misdivision in wheat in subsequent papers (48, 49, 50). In the 1943 report he states that various isochromosomes in wheat frequently misdivide at Anaphase I when they are unpaired.

Smith (79) studied two fragments of a chromosome in Triticum monococcum L. (2n = 14) that apparently arose as the result of breakage at the centromere. The fragments were discovered in an individual offspring of a spike that had developed on a plant grown from an X-rayed dormant seed. The shorter of the two fragment chromosomes was a telocentric chromosome composed of one arm of one of the normal chromosomes and the longer fragment was an isochromosome for the other arm of the same chromosome. The fragments were rarely transmitted through the pollen and through less than half the eggs. He demonstrated the usefulness of such fragments in the study of linkage relations of genes and suggested a method for associating the fragments with other chromosomes (one at a time) by means of interchanges.

Most of the work with wheat on telocentric chromosomes and isochromosomes has dealt largely with derivatives of the "C" chromosome (IX in Sears series). Sears (72) found misdivision in microsporocytes of wheat at anaphase I which occurred at a frequency sufficient to account for the frequency of telocentrics and isochromosomes observed in the progeny of monosomic plants. Sanchez-Monge and Mac Key (66) reported that misdivision of univalents occurred mainly at the second meiotic division. Li, Hsia, and Lee (46) determined cytologically meiotic misdivision of both isochromosomes IX and telocentric chromosome IX. Sears (42) found only slight differences in the female transmission and frequencies

of misdivision of univalent iso- and telo- IX in comparison with normal IX, however, both iso- IX and telo- IX were somatically unstable. Smith, Huskins, and Sander (81) reported that the behavior of iso- IX was similar to normal IX. They also noticed that the isochromosome had a smaller tendency to be excluded at T II than did normal IX; a similar observation was made by Sanchez-Monge (cited by Sears, 74). Akerman and Mac Key (66) found the isochromosome of the long arm of chromosome IX paired with normal IX in 3% of the pollen mother cells while Smith, Huskins, and Sander (81) noticed similar pairing in 48% of the pollen mother cells. Huskins (37) found pairing of isochromosomes for long arm of IX with normal IX or with a homologous isochromosome to be quite variable but never exceeding 50%.

Misdivision of univalents at T I was observed by Darlington (21) in *Fritillaria*, Upcott (103) in *Tulipa*, and by Koller (43) in *Pisum*. Sears (74) found that misdivision of univalent at T I resulted in the production of both telocentrics and isochromosomes. Misdivision of univalents at T I may be grouped according to Sears (74) into 3 categories as follows: (a) One normal chromatid passes to one pole and the two arms of the other chromatid either pass separately to the other pole or one or the other remains acentric on the plate. (b) Two identical arms pass to one pole and the other two arms either go to the other pole or one or both remain acentric on the plate. (c) Three arms go to one pole and the fourth arm either passes to the opposite pole or remains on the plate. Sears (74) working with the variety Chinese observed misdivision of the univalent- IX at T I in 39.7% of microsporocytes as compared with a total frequency of only 1.7% in the variety used by Sanchez-Monge and Mac Key (66).

Misdivision of univalents at T II has been reported by Upcott (103) in *Tulipa*, Koller (43) in *Pisum*, and by Darlington (21) in *Fritillaria*.

Sears (74) reported that at T II as at T I univalent IX of Chinese showed a higher frequency of misdivision than did the variety univalents of Sanchez-Monge and Mac Key (66); at least 29.3% of the lagging univalents in Chinese misdivided (Sears, 74) while Sanchez-Monge and Mac Key (66) report 10.7% misdivision. Sanchez-Monge and Mac Key (67) grouped misdivision at T II into two classes: (a) the two halves of the centromere separate early and lead the way to the poles, and (b) the centromere is pulled apart after the two have been carried to opposite poles. Misdivision at T II according to Sears (74) involved some of the newly formed isochromosomes as well as normal chromosomes, however, there was a high frequency of loss of T II laggards. It was observed that there was no tendency for telocentrics to misdivide or to form isochromosomes at first microspore mitosis.

Genetic tests by Sears (74) showed that in 17.8% of the eggs in monosomics of chromosome IX which transmitted a chromosome IX or derivative it was an isochromosome or telocentric for the long arm which was transmitted.

Sears (75) found no differences in frequency of formation of isochromosomes among 16 independently produced telocentrics for the long arm of chromosome IX. He observed somatic loss of both telocentrics and isochromosomes for chromosome IX and other wheat chromosomes, with more frequent loss of the telocentric.

On the basis of the work of all these investigations the mode of origin of isochromosomes and telocentrics in common wheat seems fairly well established. At first meiotic division, both telocentrics and isochromosomes are produced from univalents. At the second meiotic division some of the isochromosomes are converted to telocentrics by a second misdivision. Additional telocentrics are formed by misdivision of some of the chromosomes which divided normally at first division.

According to Sears (74) it is possible that isochromosomes actually transmitted are produced by misdivision of telocentrics at some post meiotic division.

2. Breeding Behavior of Wheat Aneuploids

A. Nullisomics

The breeding behavior of nullisomics depends on the extent of egg and/or pollen fertility. Sears (71) reported that none of the 17 different nullisomics were completely sterile, 15 or 16 were female fertile, 10 or 11 were partially male fertile, and one was male fertile only. Nullisomic wheat plants, if at least partially male and female fertile produce only nullisomic offspring when selfed (Sears 76). Progeny of nullisomic -III, which is partially asynaptic (Sears 71), may include aneuploid types other than nullisomics. In crosses with normal (disomic) lines, nullisomics produce monosomics corresponding to the respective nullisomics; nullisomic -III is an exception because asynapsis causes it to give rise to a variety of aneuploid progeny when crossed with normals. Because of depressed vigor and fertility, it is usually impractical to use nullisomics in making crosses. Only nullisomic -I, Nullisomic -VII, and Nullisomic -XXI are maintained as nullisomics, and only nullisomics -VII and XXI are used in crosses (Sears 76). For the other 19 chromosomes monosomics, monotelosomics or mono-isosomics are used instead of nullisomics.

B. Monosomics

The breeding behavior of monosomics has been studied by Nishiyama (56), Huskins (37), Smith, Huskins, and Sander (81), Sears (71, 76), and

numerous other investigators. Monosomic plants when selfed produce disomic, monosomic, and nullisomic offspring in frequencies varying with the chromosome concerned (Sears 71, 76). Sears (71) found that female transmission of 20- chromosome gametes is approximately 75% regardless of the chromosome concerned because of irregular meiotic behavior and frequent elimination of the univalent chromosome at reduction division. Male transmission of the deficiency varies from approximately 1% for several nullisomics to approximately 10% for nullisomic -III (Sears, 76). The 21- chromosome male gametes account for from approximately 90% to 100% of the fertilizations presumably because competition favors the 21- chromosome gametes. When monosomic plants are used as females in crosses with normals approximately 75% of the offspring are monosomic, when used as males about 4% of the progeny are monosomic. Table I illustrates the breeding behavior of monosomic plants.

TABLE I

FREQUENCIES OF DISOMIC, MONOSOMIC, AND NULLISOMIC OFFSPRING EXPECTED IN F_2 FROM SELFING TYPICAL MONOSOMIC PLANTS, i.e. 4% TRANSMISSION OF 20- CHROMOSOME GAMETES THROUGH THE MALE, 75% THROUGH THE FEMALE.

Transmission through the female	Transmission through the male	
	21- chromosome pollen (n) 96%	20 chromosome pollen (n-1) 4%
21 chromosome eggs (n) 25%	21" plants (disomic) 24%	20" 1' plants (monosomic) 1%
20 chromosome eggs (n-1) 75%	20" 1' plants (monosomic) 72%	20" plants (nullisomic) 3%

Totals - 21" plants - 24%

20" 1' plants - 73%

20" plants - 3%

C. Monotelosomics and Mono-isosomics

In the production of substitution lines ordinary monosomics cannot be used because of the possibility of obtaining monosomics deriving their univalent chromosome from the female instead of the male parent. However, if the male parent is allowed to self between successive backcrosses there would be no possibility for the monosomics to obtain their monosome from the female parent and monosomics could be used as females. Monosomics are available, having a telocentric chromosome or an isochromosome instead of a normal whole univalent chromosome, these can be cytologically recognized (Sears 71, 72, 76). The monotelosomics or mono-isosomics can safely be used in the development of substitution lines, Sears (76). Since the male and female transmission frequencies of telocentrics and isochromosomes are not yet known no definite F_2 ratios can be predicted for offspring of monotelosomics or mono-isosomics that are selfed. The F_2's of selfed monotelosomics or mono-isosomics should, however, be composed of 3 types of individuals: (1) nullisomics

(11) monotelosomics or mono-isosomics

(111) di-telosomics (20" + one pair of telocentric chromosomes) or di-isosomics (20" + one pair of isochromosomes).

3. Cytogenetic Methods of Analysis in Common Wheat Using Aneuploids.

A. Absence of Genetic Effects in Nullisomics

This method of analysis can be used to locate dominant genes and certain types of recessive genes in any variety in which nullisomics have been established.

These genes can be located simply by observing the absence of their effect in the proper nullisomic. Sears (71) using nullisomic analysis in the variety Chinese located several dominant genes. A gene for red seeds was associated with chromosome XVI; the chromosome which is absent in nullisomic XVI. Nullisomic XVI produces seeds that are white. Two dominant awn inhibiting genes were found to be located on chromosomes VIII and X because of increased awn development in nullisomics VIII and X. Two awn promoting genes were found to be located on chromosomes II and XX - this was shown by the complete awnlessness of nullisomics II and XX. Sears (73) using nullisomics and working on the inheritance of the _sphaerococcum_ gene in wheat showed that there is a class of dominants which cannot be located using nullisomics because the critical nullisomic still shows the dominant phenotype. In crosses of _T. sphaerococcum_ with 17 different nullisomics of Chinese, no F_1 (all monosomic) was of the _sphaerococcum_ type, although, the _sphaerococcum_ gene must have been in the hemizygous condition since it was located on one of the 17 chromosomes tested. In F_2 families involving chromosome XVI, segregation was not at random, the disomics were _sphaerococcum_ while monosomics resembled _T. vulgare_. The results show that the dominant allele of the _sphaerococcum_ gene is carried by chromosome XVI of Chinese. There is, however, no tendency for Chinese nullisomic XVI to resemble _T. sphaerococcum_ since two doses of the _sphaerococcum_ gene are needed for development of this character, and the gene in the hemizygous state is relatively ineffective.

The corresponding type of recessive gene, if present in Chinese can be located by observation of nullisomics or monosomics. These recessive genes are ineffective in the hemizygous condition. Sears (71) located the recessive squarehead and speltoid-supressing genes on chromosome IX by observing the absence of the characters in both mono-IX and nulli-IX.

These hemizygous-ineffective recessives express themselves only in double or greater dose.

B. F_2 Analysis of Monosomic F_1's

Dominant, ordinary recessive, and hemizygous ineffective recessive genes can be studied in the F_2 populations.

If a simple dominant gene conditions a character, the critical F_2 family contains 1 to 10% of the plants with the recessive character. This deviation from the 3:1 ratio occurs because both disomic and monosomic plants carry the dominant gene(s) and only the nullisomic plants express the recessive form of the characteristic. Unrau (102) reported the location of two dominant genes using the F_2 method. The gene for red color of glumes in Federation 41 was found to be associated with chromosome I. One simple dominant gene in Hymar for dense spikes was associated with chromosome XX. Transgressive segregation indicated that at least 1 additional gene was modifying the degree of spike density. Sears (76), using F_2 analysis, reported that the pubescent-glumed gene in Indian was associated with chromosome XIV.

The F_2 method is also applicable to location of two or more complementary or duplicate genes located on different chromosomes. Clausen and Cameron (19, 20) located duplicate genes for chlorophyll production in <u>Nicotiana Tabacum</u>. Larson (45) in crosses of Chinese with S-615 using aneuploid analysis and relying mainly on F_2 data, associated four genes affecting stem solidness with chromosomes VIII, XIII, XIX, and XX. The gene for promoting solidness was associated with chromosome VIII and solidness inhibitor genes were associated with chromosomes XIII, XIX, and XX of Chinese. Unrau (102) located one of two duplicate genes for winter

habit of growth in Hymar with chromosome IX.

Duplicate or complementary genes carried by the same chromosome can be located by F_2 analysis. Sears and Rodenhiser (77) found that two dominant complementary genes for resistance of the variety Timstein to stem-rust race 56 were located on chromosome X. All the families, except the chromosome family, segregated approximately 9 (resistant) : 7 (susceptible). In F_2 populations of chromosome X, 122 plants were resistant and only 2 (presumably nullisomic) were susceptible.

C. F_3 Analysis

In this method, F_3 populations from selected disomic F_2 individuals are studied. Sears (76) discusses the use of the method in locating genes. He states that it may be advisable to use this method if it is not possible to score F_2 populations, or if it is desired to locate several genes requiring test procedures. In critical F_3 populations, all of the disomics will be homozygous for the gene under study, and the chromosome is then designated as the bearer of that gene or those genes. No genes have been located using this method.

D. Use of Chromosome Substitution Lines

(a) From other Wheat Varieties

The use of this method in locating genes has been discussed by Sears (71, 76). Sears (76) states that chromosome X of Timstein has been substituted for chromosome X of Chinese and that it was possible to establish that this chromosome controls resistance to everyone of the several rust races tested. This method of analysis was employed in studying the genetics

of characters reported on in this study; further discussion of the method, in common wheat, will follow the results in this report.

(b) Alien Chromosome Substitutions

O'Mara (58) studied the effect of substituting a specific *Secale cereale* chromosome for a specific *Triticum vulgare* chromosome. Nullisomic IX plants are completely male sterile, largely female sterile and weak. Adding the *Secale* chromosome in the disomic condition to nullisomic-IX, which is equivalent to substituting it for chromosome IX, restores male sterility, increases female fertility and improves plant vigor so that individuals appear normal. This effect is different from that of adding the bivalent to the normal *T. vulgare* complement which results in semi-dwarf partially female fertile plants. His observations show that effects of substitution cannot be predicted from addition.

Gerstel (28) discusses the mechanism of chromosome substitution in backcrosses of the *N. Tabacum* - *N. glutinosa* amphidiploid to *N. Tabacum*. It was found that Holmes substituted a chromosome from *N. glutinosa*, which carried genes for mosaic resistance, for one of *N. Tabacum*.

4. Genetics of Characters Involved in this Study.

A. Awning

Since the first genetic study on the inheritance of awning in common wheat hybrids was reported in 1905 by Biffen there has been lack of agreement amongst investigators on the genetics of awning. Monogenic, digenic, trigenic and tetragenic control of awning has been reported. Some of the reasons why there have been so many discrepancies in the results obtained may be due to (1) the use of different classification systems, (11) the crossing of material similar in phenotype but different in genotype and (111) the incorrect classification and grouping of individuals in segrega-

ting generations. Most authors have regarded the awnless or tip awned condition as being dominant to awned, however, the antithetical view has also been taken, Howard and Howard (39), Stewart (84), etc.

Monogenic ratios have been obtained by numerous investigators in crosses of awnletted or tip-awned with fully awned varieties, Ausemus (5), Biffen (6), Clark and Quisenberry (14), Gaines and Singleton (27), Goulden, Neatby and Walsh (30), Neatby and Goulden (53), Quisenberry (63), Quisenberry and Clark (64), Shen, Tai and Chang (78), Stewart (87), Stewart and Bischoff (88), Stewart and Dalley (89), Stewart and Tingey (94), Torrie (100), Swenson, Buchholtz and Grafuis (96).

The awnless condition was found to be dominant or incompletely dominant, also, the awned condition was never completely recessive. The F_1 plants of these crosses have awn tips distinctly longer than the awnletted or tip-awned parent but nearer to it than to the awned parent. The F_1 plants were not of exactly the same awn type in all these crosses. In some cases they had awn tips distinctly longer than those of awnletted or tip-awned parent and it was possible to classify F_2 into a 1:2:1 ratio. In others, the heterozygote could only be distinguished from the homozygous awnletted plants by their breeding behavior, and the F_2 was classified in the ratio 3 (awnletted) : 1 (awned).

Several workers have studied the genetics of completely awnless wheats. Digenic ratios have usually been obtained in crosses of awnless with tip-awned or completed awned varieties. Ausemus (5) reported that two factor pairs are involved in awn inheritance in the cross Hope (awned) x Supreme (awnless). Clark (9) in a cross of Kota (awned) x Hard Federation (awnless) explained inheritance on the basis of a dihybrid ratio in which 5 classes were studied and the short-awned and awned classes were shown to be recessive to the awnless, apically awnletted and awnletted classes. Clark,

Florell and Hooker (12) studied awn inheritance in crosses between Bobs (awnless) and Hard Federation (awnless) with Propo (awned). F_1 in both crosses was apically awnletted showing that awnlessness is dominant. The F_2 and F_3 segregated into 5 classes. A 9:7 two factor F_2 ratio was obtained in both crosses. Clark, Quisenberry and Powers (15) in a cross of Hope (awned) x Hard Federation (awnless) showed that 2 pairs of genes condition awning. Hope was postulated to have the genotype aabb and Hard Federation the genotype AABB. Love and Craig (51) reported a 15:1 ratio for tip-awned and awnless to awned in a cross between Sonora (awnletted) and other awnless varieties. The results indicated that Sonora carries a factor for awns. Quisenberry and Clark (64) made crosses of Sonora with Quality (awnletted), Supreme (awnless) and Reliance (awned). In the Sonora x Quality cross a complete range of segregation was obtained in the F_2 from awnless to awned. On the basis of F_2 and F_3 results it was assumed that each variety carried a dominant awn inhibiting gene and the genotype of Sonora was aaBB and Quality AAbb. In the Sonora x Supreme cross segregation in F_2 and F_3 indicated a single factor difference, Supreme was assumed to have the genotype AABB. From the cross Sonora x Reliance segregation could not be explained by a single gene difference, a minor gene appeared to be operating. Reliance genotype was assumed to be aabb. Stewart (84) in crosses between Federation and awned varieties as Sevier found that the 2 awn genes of Federation were linked with 35% c/o. In another Federation cross Stewart and Heywood (90) found the 2 genes for awnlessness segregating independently. Gfeller (29) studied awn inheritance in a Garnet x Red Fife cross; F_2 and F_3 results gave a dihybrid ratio of 5 awnless : 5 apically awned : 5 awnletted : 1 awned. The parents carry different genes which behave cumulatively in inhibiting awn expression. In a Hard Federation (awnless) x Kota (awned) cross,

Stewart and Judd (91) concluded on the basis of F_2 and F_3 results that 2 independently inherited gene pairs are responsible for awnedness. Kilduff (42) in a Kota x Garnet cross concluded that at least 2 gene pairs conditioned awning.

The work of Watkins and Ellerton (105), one of the most extensive studies conducted on the genetics of awning in wheat, shows three or possibly four main loci affecting length of awn. At one locus, B_1 and $b_1{}^a$ reduce the awns to tip awns or half awns and are dominant to over the non-inhibitory allele, b_1. At another locus are alleles B_2 and b_2, similar in effect to B_1 and b_1. A factor $b_2{}^a$ or A, similar to $b_1{}^a$, seems to belong to this series but may lie at a separate locus. The Hd (hooded) factor reduces the awns and makes them twisted or curved. All these factors are in the A and B genomes. They postulated that either one of the 3 genes, B_1B_2 or A in the homozygous state produces tip-awns. If any 2 or all 3 of the genes are in the homozygous dominant state the plant is awnless. When all 3 genes are in the homozygous recessive state the plant is awned. There are several factors in addition to the ones described according to Watkins and Ellerton (105) which affect awn length to a greater or lesser degree. The main effect of these genes is on some other character, such as spike density or glume length.

Clark, Florell and Hooker (12) studied awning in crosses between awnless Bobs and Hard Federation with awned Propo. They stated that as many as 4 factor pairs are involved in the inheritance of awning.

Using nullisomic analysis in the variety Chinese Sears (71) located several genes affecting awning. Hd (hooded) was found to be located on chromosome VIII, B_2 was associated with chromosome X and b_1 with chromosome IX. Two awn promoting genes were associated with chromosomes II and XX. O'Mara (58) using deficiencies was able to associate 3 major awn inhibiting genes with chromosomes VIII, IX and X. In crosses of Chinese

with Hymar (both almost awnless), Unrau (102) found that awning was conditioned by 3 genes. Chromosomes VIII and X of Hymar carried recessive alleles of the 2 dominant awn-inhibiting genes of Chinese. A dominant awn inhibiting gene with greater effect than either of the 2 Chinese awn inhibitors was associated with chromosome IX of Hymar. Unrau's results supplement the previous findings of Sears (71) and O'Mara (58). Heyne and Livers (34) using monosomic analysis studied awning in the variety, Pawnee. They proposed a series of "A" genes, in addition to the series already present, to explain awning in their crosses. An "A" gene is (hypothetically) incompletely dominant over an awn producing allele a. The recessive gene a in the homozygous condition could theoretically produce full awns if not inhibited by partially epistatic genes Hd or B_2. Assigning a_1 and a_2 to chromosomes II and XX of Chinese and assigning similar genes to chromosomes XII, XVI and XXI of Pawnee the genotypes of Chinese and Pawnee would be as follows: Chinese Hd(8) B_2(10) a_1(2) a_2(20) A_3(12) A_4(16) A_5(20) and Pawnee hd(8) b_2(10) a_1(2) a_2(20) a_3(12) a_4(16) a_5(21). From these studies it appears that chromosomes XII, XVI and XXI are involved in awn expression as well as chromosomes II, VIII, IX, X, and XX.

B. Earliness

Although most investigators claim earliness is governed by a complex factor relation, monogenic, digenic and trigenic inheritance has been reported.

Biffen (6) in an interspecific cross between Polish, an early wheat, and Rivet, a late wheat, reported that one factor pair governs the inheritance of earliness in wheat and that earliness was dominant. Florell (23)

crossed Marquis x Sunset (very early) and found that one factor pair is responsible for earliness. There was no genetical overstopping the early or late parental limits by any of the hybrid populations. Earliness showed dominance in the F_2 generation. Florell suggested the possible presence of a number of minor modifying gene pairs.

Nieves (54) in a cross of Kanred x Florence found the early heading date of Florence in F_1 to be dominant but in later generations to be intermediate. Three gene pairs conditioned earliness. Nieves (55) observed that the F_1 of Florence x Barletta headed on the same day as the early parent, Florence. In later generations segregation showed earliness to be controlled by 3 independent gene pairs.

Thompson (98) studied earliness in a number of spring varieties. F_1 plants matured with the late parents while the ranges in F_2 extended in all cases at least as far, in either direction, as the means of the 2 parents. Thompson (98) showed that multiple genes are concerned with earliness directly and in addition many factors may affect earliness indirectly i.e. a factor causing a short stem may cause a shorter ripening period. Transgressive segregation was observed in some F_3 families which were earlier than the early parent. Clark (9) reported that in a cross between Kota and Hard Federation earliness was dominant over lateness. Clark (10) reported on studies in crosses between Marquis and Hard Federation in which he found early heading partially dominant in F_2. Transgressive segregation for lateness was shown in the F_3. Harrington (32) in crosses between varieties of durum wheat concluded that multiple genes control inheritance of earliness. Clark and Hooker (13) reported that in the F_2 of Marquis x Hard Federation, early heading was partially dominant although no large early and no small late groups appeared. Stephens (83) studied earliness in 6 varieties of spring wheat. F_2 and F_3 data indicate that

earliness may be due to a number of independent multiple genes having a cumulative effect. In one of the crosses there was evidence of transgressive segregation as the extremes of both parents were exceeded. A study of earliness was made by Aamodt (1) in diallel crosses of Marquis, Kota and Kanred. Earliness was dominant to lateness. The data indicated that at least 2 gene pairs conditioned this character. It was suggested that the genotype of the late heading Marquis x Kanred hybrid would be AAbbccdd, when crossed to Marquis (probably AABBCCDD) the F_1 will be AABbCcDd. It would be an early spring type. The actual results in the F_2, 15 (early) : 1 (late) fitted fairly well the theoretical expectations according to the proposed hypothesis. Florell (24) studied earliness in the F_1 of the backcrossed generation in Quality (T. vulgare) x Jenkin (T. compactum) and in Jenkin x Little Club (T. compactum). It was found that probably 3 or more factors are responsible for the differences in earliness observed. Waldron (104) found Marquis significantly earlier than Kota. Selection 1656 and Ceres are both earlier than Marquis by an amount more significantly greater than Marquis is earlier than Kota. Selections made from 1656 indicate that in this selection there are at least 2 pure breeding transgressive segregates for earliness. On the basis of these results it was assumed Kota and Marquis to be separated by at least 4 pairs of alleles. Torrie (100) studied earliness in F_2 and F_3 generations of the crosses, Selection I-28-60 x Milturum, Reward x Caesium, and Caesium x Marquis. Multiple genes were found to control inheritance of earliness. A partial dominance of earliness was found in the crosses Reward x Caesium and Caesium x Marquis. Gfeller (29) reported that the F_1 of a cross between the early parent Garnet and the late parent Red Fife was intermediate in earliness. A unimodal F_2 segregation was obtained showing the presence of the action of many genes governing earliness.

Shen, Tai and Chang (78) studied earliness in a cross between a Chinese variety, Pathology 4592 and an Australian variety, Nebawa. Date of heading of F_1 plants covered practically the whole range of the 2 parents with a mean close to the early parent. A number of F_2 plants headed earlier than the early parent but no plants headed later than the late parent. F_3 results showed that some plants in at least 2 and possibly more lines were genotypically slightly later in heading than the late parent. The number of genes involved in the cross could not be determined with certainty but it was concluded that multiple genes with minute effects were involved. The early genes were found to be partially dominant over the late genes. The same authors in a cross of Prelude x Nanking 2905 obtained transgressive segregation.

Freeman (25) in a cross between durum and common wheat, found in the F_2 and F_3 that the average date of heading, while intermediate was nearer that of the late parent indicating that lateness is at least partially dominant. Bryan and Pressley (8) crossed Sonora and Turkey wheats and observed that the F_1 was intermediate in time of heading between the parents and the majority of the F_2 was inclined towards the late parent. They found that lateness was partially dominant.

C. Plant Height

Few investigations have been conducted on the genetics of plant height. Digenic as well as multigenic ratios for this character have been reported.

Nieves (54) reported that in the cross Kanred x Florence, tallness was dominant and bifactorial. Nieves (55) again reported on the genetics of plant height in 2 different crosses. In the Florence x Kanred cross, tallness introduced by Kanred was dominant as reported in 1936. It was suggested that two independent gene pairs controlled plant height.

In the Barletta x Florence cross, dwarfs appeared in certain F_2 families in the ratio 3:13. Barletta is thought provisionally to be doubly recessive and Florence doubly dominant for genes conditioning plant height. The results suggest the existence of a dominant N gene for tallness, which also acts as an inhibitor of E. All dwarf F_2 plants were sterile and the hypothesis could not be checked.

Freeman (25) in a durum common wheat cross found the F_1 hybrids taller than the tallest parent and a wide range of segregation for height was observed in the F_2. There was greater variability in the shorter progenies indicating complex inheritance. Harrington (32) in Mindum x Pentad crosses found no F_3 lines exceeding Mindum (40.3") in height, but 6 lines were shorter than Pentad (34.6") indicating the presence of more than one pair of genes for height. Clark (9) in Kota x Hard Federation crosses found tallness to be partially dominant. He stated that tallness was due principally to heterosis and was easily affected by environmental conditions. Torrie (100) studied inheritance of plant height in F_2 and F_3 of three different crosses, Reward x Caesium, Caesium x Marquis, and Selction I-28-60 x Milturum. Tallness was shown to be partially dominant in the cross, Reward x Caesium. Polymeric factors were thought to control the inheritance of plant height.

D. Lodging

Few studies have been conducted on this quantitative character.

Harrington (32) studied lodging resistance in hybrid families of 2 Triticum durum crosses, namely: (1) Kubanka No. 8 x Pentad and (11) Mindum x Pentad. Kubanka and Pentad are very similar in erectness, their means both being 70%, Mindum averaged 80%. Transgressive segregation took

place in both crosses. Some Kubanka 8 x Pentad lines appeared to be less erect and others considerably more erect than either parental variety. Three F_3 Mindum x Pentad lines were lower than Pentad in % erectness, and 3 were higher than Mindum. The results of these crosses indicated that erectness is dependent on several heritable factors.

Kilduff (42) conducted genetic studies in F_2, F_3, and F_4 on the progeny of 2 common wheat crosses, Kota x Red Bobs and Kota x Garnet. Two main gene pairs appeared to condition the difference in straw strength between Kota and Garnet. The entire expression of straw strength, however, could best be explained on the basis of several gene pairs. Transgressive segregation in the direction of greater weakness of straw was noted.

Genetic studies by Torrie (100) were made in the F_3 and F_4 generations of the crosses, Reward x Caesium and Caesium x Marquis. The lodging index was used to obtain the straw strength of each line. Index was calculated by the formula: $\frac{\text{\% plants lodged x Average angle off the vertical}}{90.}$

A partial dominance of strong straw was found in both crosses. On the basis of results obtained it was postulated that multiple genes apparently control the inheritance of straw strength.

E. Protein Content

Protein, a component of quality, has been studied fairly extensively. Both monogenic and multigenic control of protein content have been reported.

Worzella (106) reported the only case of monogenic control of protein content in hybrids originating from a soft red winter wheat cross involving the varieties Trumbull and American Banner.

Zinn (108) found crude protein content to be an inherent varietal

characteristic, since he obtained an interannual correlation coefficient of 0.38 in a study of 40 pure lines of wheat. Clark (10) obtained transgressive segregation for protein content beyond the upper extremes of both parents in the F_4 of reciprocal crosses of Kota x Hard Federation. Clark (10) studied inheritance of protein content in Marquis x Hard Federation and Hard Federation x Propo crosses. The F_2 hybrids of Marquis x Hard Federation were found to be intermediate with respect to the parents in protein content. The hybrids were nearer the parent of lower average protein content. F_2 and F_3 data indicated, as a whole, that crude protein content was inherited in degrees intermediate to the parents. Its mode of inheritance could not be determined. Protein content is easily affected by the environment and increased yield usually causes a decrease in protein content. In Hard Federation x Propo crosses, F_2 hybrids tended toward the low protein parent, Propo, indicating a dominance of the genes for low protein content. His data indicated that the inheritance of protein is very complex, and easily influenced by the environment. Clark and Smith (16) studied crude protein content inheritance in Nodak and Kahla durum wheat crosses. In comparison with the parents, crude protein content of F_3 strains was intermediate with an indication of transgressive segregation beyond that of the parents for both high and low protein content. Worzella (106) reported on crude protein content inheritance in crosses involving American Banner, Trumbull and Michikof. Results indicated that the mode of inheritance of crude protein content is conditioned by multiple genes. Hybrids were intermediate between the parents with lines varying in percent protein from the lower to the higher parent. Worzella and Cutler (107) found protein content to be definitely inherited in soft red winter wheat. The distribution of the hybrid populations formed a normal curve, suggesting that multiple genes controlled inheritance. Inheritance of protein content in crosses of Marquis and

Kota Spring wheats was reported on by Clark and Quisenberry (14). They found that in the F_2 and F_3 the average crude protein content was not significantly different from that of the lower protein, Marquis, parent. Several F_3 strains had a lower protein content than Marquis indicating transgressive segregation. Clark and Hocker (13) in reciprocal crosses of Marquis x Hard Federation found protein content for F_2 and F_3 of hybrids was intermediate between that of the parents and there was no indication of transgressive segregation. They state that protein content is inherited in intermediate degrees between the 2 parents by means of multiple genes. Correlations between the protein content of F_2 and F_3 were not significantly different, this illustrates how readily this character is influenced by the environment. Aamodt and Torrie (2) found inheritance of protein content in the Milturum x Selection I-28-60 cross to be controlled by multiple genes, whose exact nature was not determined. Clark, Florell and Hooker (12) in a series of crosses between Bobs, Hard Federation and Propo, found a tendency for low protein content to be dominant. Correlations between F_2 and F_3 were not significant. Multiple gene mode of inheritance was postulated which is in agreement with the results obtained by Clark and Hooker (13).

F. Spike Density

Although a few investigators report digenic and multigenic control of spike density, in general, simple segregation has been observed in genetic studies of this character.

Most investigators agree that one main gene is responsible for differentiating the dense spiked from lax spiked plants. Biffen (6) in crosses between Rivet x Polish, and Devon x Hedgehog obtained 1:2:1 and 3:1 segregation ratios respectively. Lax spikes appeared to be dominant

to dense spikes, Boshnakian (7) obtained ratios which approached 3 dense: 1 lax. The F_3 showed various degrees of density within the dense and lax forms. These variations were thought to be the result of segregation of modifiers or of additional density factors capable of producing density only within short ranges. Spike density was studied by Florell (24) in the crosses, Quality x Little Club, Quality x Jenkins, Jenkins x Hard Federation, and Jenkins x Marquis. A one factor difference between the club and lax types of a pike was found in the backcrosses of the 4 varietal combinations and the results were verified in the regular F_2 and F_3 generations. In the F_3 generations both club and lax segregates of different densities were observed. Minor genes evidently were present. Gaines (26) crossed numerous varieties and explained his ratios by assuming a one-factor difference. Schlehuber (68) in crosses Albit x Minhardi and Albit x Buffum reported a one gene 3:1 ratio for both crosses. Stewart (84) found a ratio of one dense to two haterozygous to one lax in his studies of spike density in wheat hybrids. He reported transgressive segregation for spike density in both directions and gives no genetic hypthesis. Similar results for spike density were obtained by Stewart in (85) and (86) and (87). Other investigations reporting segregation of spike density into simple 1:2:1 ratios were published by Stewart and Bischoff (88), Stewart and Heywood (90), Stewart and Price (93), Stewart and Woodward (95), Stewart and Dalley (89), and Stewart and Nelson (92). In most of these investigations transgressive segregation in both directions were observed. The results show that one or more minor factors modify the expression of the major gene.

Meyer (24), found a digenic difference in vulgare hybrids involving crosses between the fairly dense squarehead type of wheat and the lax long-spiked varieties. Elliott (22) also found the results of F_1,F_2,F_3 and

F_4 of T. vulgare (Sonora) x T. compactum (Club C.I. 4534) for spike density to be controlled by 2 genes. One gene inherited from Sonora, exerted a greater influence, while the gene from the Club parent seems to have a less marked effect upon the length of spike. Nieves (54) in the cross Kanred x Florence showed a 9:7 digenic ratio with transgression for spike density in the F_2. In 1937 (Nieves) reported the results of a cross between Florence and Kanred, both medium dense. Forms denser than the parents appeared in the F_2 in the ratio 9:7, each variety appears to be homozygous for one of two independent dominant density genes.

Nilsson-Ehle in 1911, according to Hayes and Garber (33) studied spike density in crosses between compact and middense wheats. The F_2 segregated into compact, middense and lax forms. He assumed the dense form was of the genotype $CCL_1L_1L_2L_2$. The C gene was thought to inhibit the expression of the lengthening genes L_1 and L_2 and also to produce spikes with short internodes.

Unrau (102) in crosses between Chinese monosomics (lax) and Hymar (dense) associated the gene for spike density with chromosome XX. Transgressive segregation indicated that at least one additional gene was modifying the degree of density.

G. Thousand-Kernel Weight

Differences in thousand-kernel weight have been found to be definitely inherited. Monogenic, trigenic and multigenic inheritance has been reported.

Jasnowski (40) in crosses between three varieties of T. vulgare showed that three pairs of cumulative genes are concerned with the inheritance of grain weight. There was no correlation between weight of

grains and number of grains per spikelet or number of spikelets per spike but weight of spike was found to be depdendent on weight of grain. Studies on the progeny of crosses (Jasnowski, 41) between Suska, Chinese, and Hildebrandt's indicated that three pairsof cumulative genes were involved. The genotypes of the varieties studied were designated thus: Suska aaBBcc, Chinese AAbbcc, Hildebrandt's AABBCC.

Worzella (106) reported that differences in thousand kernel weight in hybrids of American Banner x Trumball appeared to be monogenically controlled.

Worzella and Cutler (107) studied thousand kernel weight in soft red winter wheat and found the characteristic to be definitely inherited. The distribution of the hybrid populations studied formed normal curves, and suggested multiple gene inheritance.

H. Yield

Yield has been found to be a definite heritable character. Its expression, however, is influenced to a large extent by environmental conditions.

Waldron (164) found yield of Ceres, a selection from a Marquis x Kota cross to be significantly higher than that of either parent. Ceres is a transgressive segregate with regard to yield, this effect was stated as being due to the additive effect of high yielding genes obtained from each parent. Clark and Smith (16) studied yield in F_2 and F_3 of Nodak x Kahla durum wheat crosses and found the yield of F_3 plants to be intermediate between the parents with certain F_3 strains showing transgressive segregation by exceeding the yield of the best parent checks. Their results showed partial dominance of high yield. Clark (9) states that

"yield may be considered as a character complex affected by environment and by most of the morphological and physiological characters of the plant". Yield appeared to be due to multiple genes in the Kota x Hard Federation cross. A partial dominance of the high yielding parent was obtained. Clark and Hooker (13) reported transgressive segregation for grain yield in a Marquis x Hard Federation cross. Similar results were obtained by Clark, Florell and Hooker (12) in crosses between Bobs, Hard Federation and Propo wheats. Clark, Quisenberry and Powers (15) studied yield inheritance and found partial dominance of high hield, also they reported transgressive segregation for inheritance of grain yields. Aamodt, Torrie and Wilson (3) in crosses between Reward and Milturum spring wheats observed that yield appeared to be of a complex nature. A partial dominance of low yielding genes was indicated. Torrie (100) studied yield inheritance in F_3 and F_4 in the cross Reward x Caesium and reported that multiple genes apparently control inheritance of grain yield. Low yield was observed to be partially dominant.

III. MATERIALS AND METHODS OF PROCEDURE

1. Description of Parental Varieties.

The substitution lines used in this study were established by E. R. Sears. Four varieties of common wheat were involved in the production of the 3 sets of substitution lines. Chinese was used as the recipient variety and 3 sets of substitution lines with chromosomes from the varieties Thatcher, Hope, and Timstein were produced in each of the 3 sets respectively.

A description of the varieties with respect to the characters studied is given below.

Character \ Variety	Chinese	Thatcher	Hope	Timstein
Awning	awnless	awnleted	awned	awnletted
Earliness	late	early to midseason	midseason	early
Density	3.17	2.21	2.15	1.91
Height	midtall	short to midtall	midtall	short
Lodging resistance	very susceptible	very resistant	medium to strong resistance	resistant
*Protein content	13.85%	14.90%	13.35%	13.25%
*Thousand-kernel weight	22.7 grams	31.3 grams	36.5 grams	35.6 grams
*Yield	473.8 grams per 4-row rod long plot	1013.8 grams per 4-row rod long plot	675.8 (1954) grams per 4-row rod long plot	957.9 grams per 4-row rod long plot

* Value given for characters in Chinese are averages from the 3 sets of substitution lines over the years 1953 and 1954.

* Values for each Thatcher character are averages for 1952, 1953, and 1954.

* Values for each Hope and Timstein character are averages for 1953 and 1954.

2. Experimental Methods

A. Production of Substitution Lines

To illustrate the procedure of chromosome substitution the transfer of chromosome I from Thatcher to Chinese will be outlined using (a) nullisomics and (b) monotelosomics or mono-isosomics.

(a) Procedure using nullisomics.

(i) Nullisomic I of Chinese used as the female parent is crossed with the variety to be tested (Thatcher).

Nullisomic - I (20") x Normal Thatcher (20" + 1")

gametes 20' x 21' ⟶ 20" + 1' (monosomic for Thatcher one chromosome).

(ii) The monosomic F_1 plants are next crossed, as males, to nullisomic - I. Because the monosomic plants produce two types of gametes, two types of progeny are produced. From the union of 20 chromosome male and female gametes nullisomic plants are produced. When 21 chromosome male gametes unite with 20 chromosome female gametes, monosomic backcross I progeny are produced. In these plants chromosome I of Thatcher will be present as a univalent. Approximately 90 - 99% of the offspring of a nullisomic (♀) x monosomic (♂) cross are monosomic. The reason for the high proportion of monosomic plants is that approximately 90 - 99% of the functioning pollen has 21 chromosomes.

	Nullisomic - I		Monosomic F_1's		
gametes	20'	x	21' ⟶ 20" + 1'	(Thatcher)	90 - 99%
	20'	x	20' ⟶ 20"		1 - 10%

(iii) The procedure in (b) is repeated for 5, 6, or more backcross generations to nullisomic - I of the recurrent parent variety, Chinese. By the fifth backcross generation approximately 97% of the genotype will be that of the recurrent parent other than chromosome I which will be

genetically as it was in the donor variety. Selfing of these fifth back-cross generation monosomics, as mentioned earlier, will result in approximately 24% of the progeny being disomic for chromosome I of Thatcher. These disomic (21") plants represent the substitution line, they may be increased and the line can be studied by comparing it to Chinese, Thatcher, and other substitution lines.

(b) Procedure using monotelosomics or mono-isosomics.

(i) Monotelosomic - I or mono-isosomic - I of Chinese used as the female parent is crossed with the variety to be tested (Thatcher).

	Monotelosomic	x	Thatcher
	20' + telocentric	x	21' ⟶ 20" + (1' telocentric, heteromorphic pair)
gametes			
	20'	x	21' ⟶ 20" + 1' (monosomic for chromosome I of Thatcher)

	mono-isosomic	x	Thatcher
	20' + isochromosome	x	21' ⟶ 20" + (1' + isochromosome, heteromorphic pair).
gametes			
	20'	x	21' ⟶ 20" + 1' (monosomic for chromosome I of Thatcher).

(ii) The monosomic F_1 plants are next crossed as males to Chinese monotelosomics or mono-isosomics. Because monotelosomics, mono-isosomics and monosomics each produce two types of gametes, four types of individuals are possible in the progeny.

	monotelosomic - I	x	monosomic F_1's
	20' + telocentric,	x	20' ⟶ 20" + telocentric
	20'	x	20' ⟶ 20"
gametes			

20' + telocentric x 21' $\longrightarrow$ 20'' + (1' telocentric, heteromorphic pair).

20' x 21' $\longrightarrow$ 20'' + 1' (monosomic for chromosome I of Thatcher).

mono-isosomic - I x monosomic F_1's

20' + isochromosome x 20' $\longrightarrow$ 20'' + telocentric

20' x 20' $\longrightarrow$ 20''

20' + telocentric x 21' $\longrightarrow$ 20'' + (1' isochromosome, heteromorphic pair).

20' x 21' $\longrightarrow$ 20'' + 1' (monosomic for chromosome I of Thatcher).

(iii) The procedure in (ii) is repeated for 5, 6, or more backcross generations to monotelosomic - I or mono-isosomic - I of the recurrent parent variety, Chinese. Remainder of procedure is similar to that of (iii) in nullisomic procedure.

Throughout the entire program of chromosome substitution the chromosomal constitution of the plants is determined cytologically by examination of pollen mother cells.

Monosomics cannot be used as females in the backcrossing program unless each backcross is interrupted by a generation of selfing. If they are used two types of monosomics are possible in the backcross program; those receiving the univalent from the male and those receiving it from the female parent. Differentiation would be impossible unless the chromosomes carried genes for some character that could be identified. Monotelosomics and mono-isosomics are available and these are used instead of the ordinary monosomics.

B. Experimental Design of Field Experiments

A randomized blocks design of 4 replicates for each substitution line with the recipient and donor varieties as checks, was used at Edmonton.

In 1952 only substitution lines involving Thatcher were available, but in 1953 and 1954 the additional substitution lines involving Hope and Timstein also were included.

At Brooks, Alberta, where experiments were conducted in 1954 only, each of the 3 sets of substitution lines were tested in a 6-replicate balanced lattice design.

Plots were comprised of 4 rows 18.5 feet long and spaced 9 inches apart. At Edmonton individual plots were separated by 2 rows of winter wheat so that lodging could be more easily and correctly estimated.

C. Methods of Collecting Data

Awning was studied in all 3 sets of substitution lines. Four classes, depending on the extent of awn development, were employed: 1) awnless, 2) awnletted, if short awnlets were present, 3) apically awned, if short awnlets were present near the base of the spike and the lenght oa awns increased towards the apex, usually the upper half being almost fully awned, 4) awned, when the spike was fully awned.

Date of heading, used as an indication of earliness, was recorded separately for each plot. The material in a plot was considered headed when approximately 75 - 80% of the leading spikes had just emerged from the boot. Heading of plants in individual plots was extremely uniform, which greatly facilitated recording these data.

Plant height, determined shortly before maturity, was recorded as the height of plants in inches from the ground to the top of the spike. The heights of 15 plants selected at random were averaged for each plot.

Spike density was determined for the leading spikes of 15 different plants in each plot. The average spike density was calculated by dividing the number of spikelets per spike by spike lenght. The length of the

spike was measured from the base of the rachis node to the tips of the uppermost spikelet not including the awns. All nodes were counted to give the true number of spikelets.

The average 1,000-kernel weight, in grams, of each line was obtained by averaging the weights from three random 200-kernel samples. The 1,000 kernel weights were calculated from a bulk sample for each line.

Lodging resistance was recorded at intervals during a period from approximately 4 weeks after heading to maturity. An average value for each plot was obtained from 6 observations.

A scoring range of 1-10 was used, with plants standing erectly being scored 1, those showing an inclination of approximately 20 degrees were scored 3-4 while plots completely lodged were given a score of 10.

Yield in grams per plot was obtained on the 2 centre rod long (16.5') rows of each plot.

Protein content was determined on random samples from each substitution line. The nitrogen content was determined using the Kjeldahl method, on 2 1-to 1½-gram ground samples from each random sample. The values of the 2 determinations were averaged and multiplied by 4.93 to give the percent protein content.

D. Statistical Analyses Of Data

Analyses of variance were computed on the data for thousand-kernel weight, yield, earliness, height, spike density, protein content, and lodging for each set of substitution lines. The character, awning, was not analyzed statistically.

IV. EXPERIMENTAL RESULTS

1. Awning

Data on the effects of whole chromosome substitutions on awning in each of the three sets of sbbstitution lines are summarized in Table 2.

Excluding the parents, three types of awn expression were found in the three sets of substitution lines. Illustrations of these awn types along with those of the recipient and donor varieties for each set are given in Figurs 1, 2, 3, and 4.

With the exception of chromosomes VIII and X there is no effect on awning by substitution of Hope chromosomes for those of the variety Chinese. Chromosomes VIII and X of Hope do, however, affect the development of apically awned plants in the recipient variety. This is as would be expected on the basis of results obtained by Watkins and Ellerton (105) who postulated $HdHdb_1b_1B_2B_2$ as the genic formula for Chinese, and Sears (71) and Unrau (102) who have shown that in Chinese Hd and B_2, two sets of dominant genes which are carried on chromosomes VIII and X respectively, reduce awn development, but do not entirely inhibit it. On this basis, then, it follows that Hope must carry the recessive alleles for increase of awn development on chromosomes VIII and X. Further, since substitution line IX is awnless as is the recipient variety Chinese it can be assumed that similar alleles are carried on this chromosome by both varieties. The question of the action of apparently recessive genes for awn development must be considered. These genes can conceivably produce phenotypic effects; they may promote awn development or they may have no effect at all. If the latter is true then the absence of awn inhibitors at the homologous or any other loci permits the expression of awns. On the basis of these results and the hypothesis stated the following genotypes and corresponding phenotypes represent the genetics of awning in this material:

TABLE 2

AWNING OF THATCHER, HOPE, TIMSTEIN, CHINESE AND THATCHER, HOPE, AND TIMSTEIN SETS OF SUBSTITUTION LINES.

Chromosome tested	Thatcher set	Hope set	Timstein set
Thatcher	awnletted		
Hope		awned	
Timstein			awnletted
Chinese	awnless	awnless	awnless
1	awnless	awnless	awnless
2	awnless	awnless	awnless
3	apically awned	awnless	apically awned
4	apically awned	awnless	awnless
5	awnless	awnless	awnless
6	awnless	awnless	awnless
7	awnless	awnless	awnless
8	awnletted	apically awned	apically awned
9	awnletted	awnless	awnless
10	apically awned	apically awned	apically awned
11	awnless	awnless	awnless
12	apically awned	awnless	awnless
13	awnless		
15	awnless	awnless	awnless
16	awnless	awnless	awnless
17		awnless	awnless
18	awnless	awnless	awnless
19	awnless	awnless	awnless
20	awnless	awnless	awnless
21	apically awned	awnless	awnless

Chinese HdHd (VIII) b_1b_1 (IX) B_2B_2 (X) awnless because of genes Hd and B_2; Hope hdhd (VIII) b_1b_1 (IX) b_2b_2 (X) awned because of absence of awn inhibiting genes; Chinese VIII Hope hdhd (VIII) b_1b_1 (IX) B_2B_2 (X) apically awned; Chinese IX Hope HdHd (VIII) b_1b_1 (IX) B_2B_2 (X) awnless and same genotype as Chinese; Chinese X Hope HdHd (VIII) b_1b_1 (IX) b_2b_2 (X) apically awned because of only one inhibitor.

When chromosomes III, VIII, and X of the awnletted variety Timstein are substituted for their respective homologous in Chinese the substitution lines carrying these chromosomes exhibit apical awnedness. The remaining sixteen substitution lines tested are as awnless as the recipient variety. Since both Chinese VIII Timstein and Chinese X Timstein show apical awnedness it seems that both chromosomes VIII and X of Timstein carry the recessive alleles hd and b_2 respectively. Chinese IX Timstein is, like the recipient variety, awnless and on the basis of this and the fact that Timstein is awnletted and carries the alleles hd and b_2, it is assumed that chromosome IX of Timstein carries the allele B_1. However it could carry another allele slightly less effective, $B_1{}^a$. On the basis of these assumptions the genotypes of Timstein and substitution lines would be as follows: Timstein, hdhd$B_1B_1b_2b_2$ or hdhd$B_1{}^aB_1{}^ab_2b_2$; substitution line VIII, hdhd$b_1b_1B_2B_2$; substitution line IX, HdHd$B_1B_1B_2B_2$ or HdHd$B_1{}^aB_1{}^a$ B_2B_2; and substitution line X, HdHd$b_1b_1b_2b_2$.

The results obtained in the set of Chinese lines with substituted Thatcher chromosomes were more difficult to interpret. Seven of the nineteen Thatcher chromosomes tested expressed awning. Chromosome III, IV, XII, and XXI substitution lines were apically awned and chromosome lines VIII and IX were awnletted the remaining twelve lines were awnless. On the basis of awn type it is assumed that Thatcher chromosome VIII carries either of two alleles, hd or Hd^a and chromosome IX carries the allele $b_1{}^a$. Chinese line X was apically awned as in the previous two sets and it seems

Figure 1. Awn types of Thatcher, Chinese, Chinese VIII Thatcher, Chinese IX Thatcher, and Chinese X Thatcher.

A. Spikes from awnleted Thatcher.
B. Spikes from awnless Chinese.
C. Spikes from apically awned Chinese VIII Thatcher.
D. Spikes from awnleted Chinese IX Thatcher.
E. Spikes from apically awned Chinese X Thatcher.

that Thatcher chromosome X carries the recessive allele b_2. The genotypes with respect to chromsomes VIII, IX, and X, for Thatcher and Chinese substitution lines, eight, nine and ten are as follows: Thatcher, $hdhdb_1^a b_1^a b_2 b_2$ or $Hd^a Hd^a b_1^a b_1^a b_2 b_2$; substitution line eight, $hdhdb_1\ b_1 B_2 B_2$ or $Hd^a Hd^a b_1 b_1 B_2 B_2$; substitution line nine, $HdHdb_1^a b_1^a B_2 B_2$; and substitution line ten, $HdHdb_1 b_1 b_2 b_2$.

The results from the three sets of substitution lines for chromosomes VIII, IX, and X substantiated previous findings. The appearance of awn types in lines carrying chromosomes III, IV, XII, and XXI of Thatcher and III of Timstein were not expected on the basis of published information. Because genes on the above four chromosomes affect awning a new hypothesis or an extension of the old one is necessary to explain the results obtained.

It is assumed that either hd or b_2 or both together are epistatic to genes on chromosomes III, IV, XII, and XXI and that Hd or B_2 or both together are non epistatic or only partially epistatic to genes on chromosomes III, IV, XII, and XXI which may be designated $K_1 K_2 K_3$ and K_4 respectively. The hypothesis holds whether the genes on III, IV, XII, and XXI are dominant or recessive. There may be more than one gene per chromosome, the assumption is made that only one gene affecting awning is present on each of the above chromosomes. We may take chromosome III of Timstein to demonstrate the hypothesis. In the donor parent genes on chromosome III are inhibited by hd and b_2. When chromosome III is substituted into Chinese the action of genes on the transferred chromosome is not inhibited because Chinese possesses Hd and B_2 and the substitution line is awned. The same explanation would hold for genes on chromosomes III, IV, XII, and XXI of Thatcher.

On the basis of this hypothesis the genotypes for Chinese, Thatcher, Timstein, and Chinese substitution lines 3, 4, 12, and 21 would be as follows:

(1) If awning genes on chromosomes III, IV, XII, and XXI are recessive

	III	IV	VIII	IX	X	XII	XXI
Chinese	K_1K_1	K_2K_2	HdHd Hd^aHd^a or	b_1b_1	B_2B_2	K_3K_3	K_4K_4
Thatcher	k_1k_1	k_2k_2	hdhd	$b_1^a b_1^a$ B_1B_1 or	b_2b_2	k_3k_3	k_4k_4
Timstein	k_1k_1	K_2K_2	hdhd	$B_1^aB_1^a$	b_2b_2	K_3K_3	K_4K_4
Subst. line 3	k_1k_1	K_2K_2	HdHd	b_1b_1	B_2B_2	K_3K_3	K_4K_4
subst. line 4	K_1K_1	k_2k_2	HdHd	b_1b_1	B_2B_2	K_3K_3	K_4K_4
subst. line 12	K_1K_1	K_2K_2	HdHd	b_1b_1	B_2B_2	k_3k_3	K_4K_4
subst. line 21	K_1K_1	K_2K_2	HdHd	b_1b_1	B_2B_2	K_3K_3	k_4k_4

(11) If awning genes on chromosomes III, IV, XII, and XXI are dominant.

	III	IV	VIII	IX	X	XII	XXI
Chinese	k_1k_1	k_2k_2	HdHd Hd^aHd^a or	b_1b_1	B_2B_2	k_3k_3	k_4k_4
Thatcher	K_1K_1	K_2K_2	hdhd	$b_1^a b_1^a$ B B or	b_2b_2	K_3K_3	K_4K_4
Timstein	K_1K_1	k_2k_2	hdhd	$B_1^aB_1^a$	b_2b_2	k_3k_3	k_4k_4
Subst. line 3	K_1K_1	k_2k_2	HdHd	b_1b_1	B_2B_2	k_3k_3	k_4k_4
subst. line 4	k_1k_1	K_2K_2	HdHd	b_1b_1	B_2B_2	k_3k_3	k_4k_4
subst. line 12	k_1k_1	k_2k_2	HdHd	b_1b_1	B_2B_2	K_3K_3	k_4k_4
subst. line 21	k_1k_1	k_2k_2	HdHd	b_1b_1	B_2B_2	k_3k_3	K_4K_4

It is believed that this or some other multiple gene theory is necessary to explain the occurrence of awn types in so many different substitution lines.

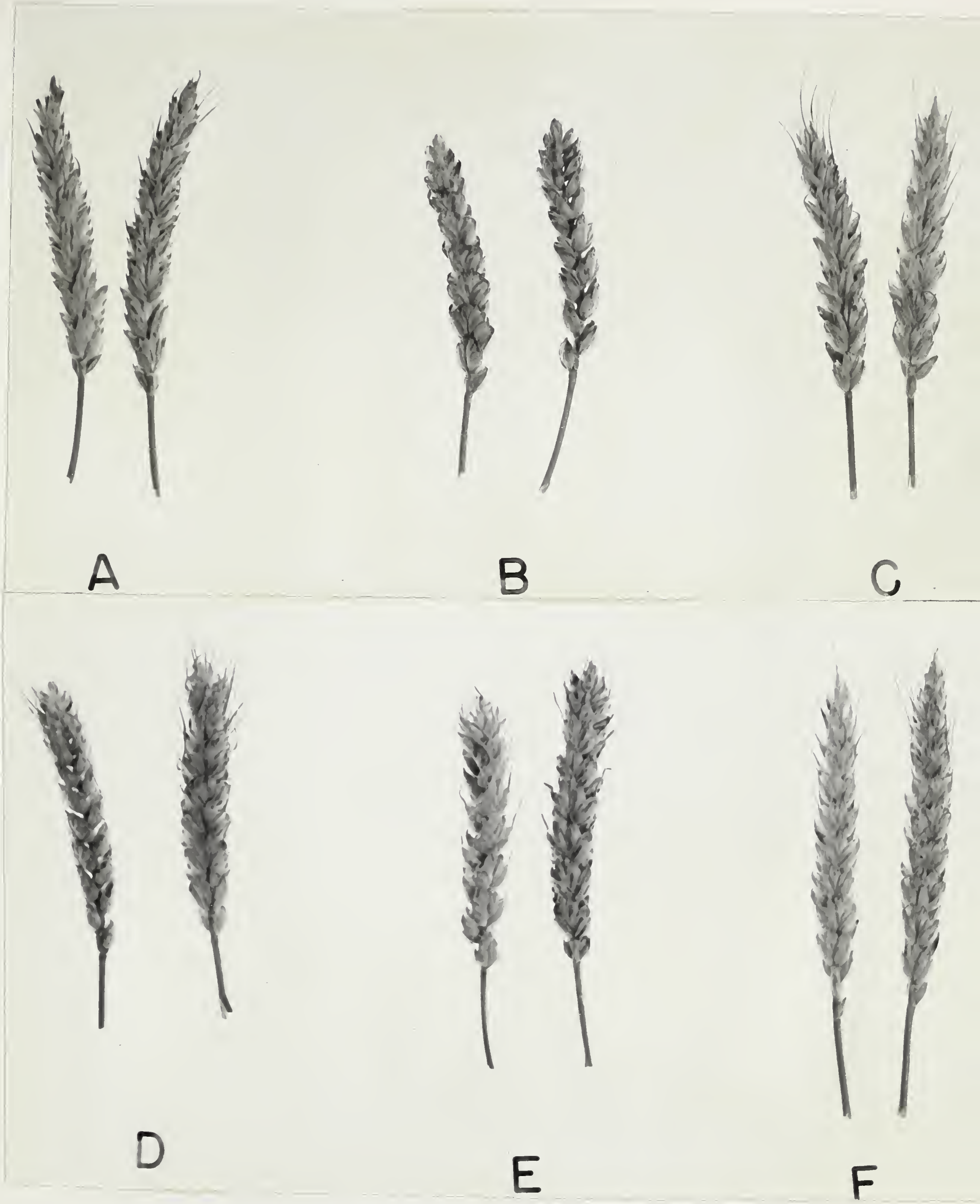

Figure 2. Awn types of Thatcher, Chinese, Chinese III Thatcher, Chinese IV Thatcher, Chinese XII Thatcher, and Chinese XXI Thatcher.
A. Spikes from awnleted Thatcher.
B. Spikes from awnless Chinese.
C. Spikes from apically awned Chinese III Thatcher.
D. Spikes from apically awned Chinese IV Thatcher.
E. Spikes from apically awned Chinese XII Thatcher.
F. Spikes from apically awned Chinese XXI Thatcher.

Figure 3. Awn types of Hope, Chinese, Chinese VIII Hope, and Chinese X Hope.

A. Spikes from awned Hope.
B. Spikes from awnless Chinese.
C. Spikes from apically awned Chinese VIII $H_o$pe.
D. Spikes from apically awned Chinese X Hope.

Figure 4. Awn types of Timstein, Chinese, Chinese III Timstein, Chinese VIII Timstein, and Chinese X Timstein.

A. Spikes from awnleted Timstein.
B. Spikes from awnless Chinese.
C. Spikes from apically awned Chinese III Timstein.
D. Spikes from apically awned Chinese VIII Timstein.
E. Spikes from apically awned Chinese X Timstein.

2. Earliness

Data on earliness in Thatcher, Chinese and Chinese lines with substituted Thatcher chromosomes are summarized in Table 3.

On the basis of the results obtained the genes on 11 of the 19 chromosomes tested, have definite and measurable effects on earliness. The effects, on earliness, of substituted Thatcher chromosomes may be divided into three classes if it is assumed that differences in earliness exceeding the 5% level are those caused by genetic effects. The chromosome classes are: (a) those hastening significantly earliness of the recipient variety, (b) those the same as or similar to Chinese, and (c) those depressing significantly the earliness of Chinese.

Thatcher chromosomes having the same or similar effect as their homologs in Chinese are IV, XI, XVI, XIX, and XXI. The interpretation of results for these chromosomes may follow either of two alternatives: (a) the genes of Thatcher are similar to those of Chinese, or (b) neither Thatcher nor Chinese carry genes, affecting earliness, on these chromosomes.

Ten Thatcher chromosomes significantly hastened earliness of the recipient variety. The degree of hastening varied with the gene or genes on the individual chromosomes. Chromosome XV hastened earliness of Chinese by approximately 1 to $1\frac{1}{2}$ days. Chromosome II, V, VII, and VIII lines were approximately 4 to $4\frac{1}{2}$ days earlier than Chinese. The most striking effects were those of chromosome lines I, III, VI, and XII which produced heading 5 to $5\frac{1}{2}$ days earlier than Chinese. These differences signify that some chromosomes have major and others minor genetic effects on this character.

The action of substitution lines Chinese IX Thatcher and Chinese X Thatcher is more difficult to assess, since these lines were more variable in their action than other chromosome lines. Chromosome IX hastened heading by 3 to 5 days except in 1954 at Brooks where it was only one day earlier.

Since the conditions at Brooks may have tended to minimize differences Thatcher IX gene or genes may be interpreted as hastening earliness. Thatcher chromosome X line was more variable than Thatcher IX line and no definite effect can be attributed to gene(s), if present, on this chromosome.

The behavior of Chinese lines carrying Thatcher chromosomes XIII and XVIII is most striking. Throughout most of the summer of each year of testing these lines behaved as true or almost true winter wheats and headed approximately 20 to 25 days later than Chinese. The behavior of Chinese XIII Thatcher was not as true as that of Chinese XVIII in that it segregated to a small extent for earlier plants. It is possible that the few early plants in this line may actually be mechanical mixtures, however, genetic segregation of hybridization with other Chinese lines or other varieties is possible. The few earlier plants do resemble Chinese in headtype, which would probably rule out hybridization with other varieties.

The genetic explanation for Thatcher chromosomes XIII and XVIII is probably as follows: Chinese on chromosomes XIII and XVIII carries dominant, spring-growth-habit genes, while in Thatcher the recessive alleles for winter habit are present on chromosomes XIII and XVIII. It has been observed that monosomic XVIII of Chinese produces considerably later heading than does disomic Chinese. When chromosome XVIII of Chinese is exchanged for chromosome XVIII from Thatcher, plants with near winter-growth-habit result.

The genetic interpretation for the results obtained may be as follows: The genes of Thatcher may be divided into two types: (a) those differentiating summer and winter growth habit, as on chromosomes XIII and XVIII, and (b) those that modify the expression of genes in (a) to a greater or lesser extent. These modifiers are not all equal in effect (Table 3);

A B

Figure 5. Photograph showing comparative earliness of Chinese and Chinese VII Hope.

A. Chinese VII Hope, headed in 60 days.
B. Chinese, headed in 67 days.

some appear to have major and others only minor modifying effects. Chromosomes I, III, VI, and XII are of the former type and chromosome XV the latter type.

Thatcher is earlier than Chinese even though it seems to carry the recessive alleles on XIII and XVIII for winter or near winter growth habit. Though the answer is unknown it seems that Thatcher possesses a larger number of both strong and weak alleles for earliness than does Chinese (10 Thatcher chromosomes hasten Chinese heading). Chromosomes I, II, III, V, VI, VII, VIII, IX, and XII are very strong modifiers and XV is a weaker modifier. The cumulative action of all these genes in Thatcher causes it to head earlier than Chinese.

Data on earliness in Hope, Chinese, and Chinese lines with substituted Hope chromosomes are summarized in Table 4.

Following a classification system similar to that used for the Thatcher set of substitution lines Hope chromosomes may be divided into two classes: (a) those the same as or similar to Chinese in earliness, and (b) those significantly earlier than Chinese.

The former class includes the gene or genes on Hope chromosomes I, VI, VIII, XI, XV, XXI, XVII, XIX, and XX. The explanations are similar to those for the lines which were non-significantly different from Chinese in Thatcher set of substitution lines.

The remaining 10 chromosomes hastened heading significantly. The most striking results were obtained with Chinese VII Hope line. This Hope chromosome hastened earliness of Chinese by approximately 10 days and the heading transgressed that of the earlier donor variety Hope. Chromosomes II, III, IX, X, XII, XVIII, and XXI hastened heading by 6 to 7 days. Chromosomes IV and V had less effect, their respective lines were significantly earlier by approximately 4 days, than Chinese. These

results show that different Hope chromosomes like those of Thatcher have unequal effects on this character (Table 4).

Data on earliness in Timstein, Chinese, and Chinese lines with substituted Timstein chromosomes are summarized in Table 5.

If it is assumed that differences in earliness exceeding the 5% level are caused by genetic effects of substituted chromosomes, two classes may be assumed (a) those producing effects the same as or similar to Chinese, (b), those producing types significantly earlier than Chinese.

Chromosome I, X, XI, XV, XVI, and XXI lines showed no significant difference in heading from Chinese. They either carry no alleles or are genetically the same as the recipient variety.

Chinese VIII Timstein and Chinese XII Timstein produced the most striking results, heading 4 to 5 days earlier than Chinese. Timstein chromosomes V, VI, and XVIII appear to possess weaker enhancing genes than VIII and XII, the respective lines headed approximately 3½ days earlier than Chinese. The group of chromosomes comprising II, III, IV, VII, IX, XVII, XIX, and XX produced minor effects, hastening earliness by approximately 1½ to 3 days over Chinese.

Since chromosome XI and XVI lines in all three sets were not significantly different from Chinese the inference may be that these chromosomes do not carry any genes affecting this character rather than possessing similar alleles. Chromosome XII of all 3 donor parents seems to possess the same allele(s). Chinese lines possessing this chromosome from the different parents hastened heading by 5 to 6 days.

That some of the homologous chromosomes of different varieties have different genetic effects is substantiated by the high significance of the lines x varieties interaction as shown in Tables 2 and 3 of the Appendix. The chromosomes having different effects are I, II, III, IV,

VI, VII, VIII, IX, X, XIX, and XXI. Taking chromosome VII as an example we see that Chinese VII Hope heads in 56.5 days whereas Chinese VII of Thatcher and Timstein head in 62.0 and 64.8 days respectively. Either a multiple allelic series for single genes are operating or chromosomes possess various combinations of same or different number of genes with or wothout differential alleles.

Earliness of individual lines was consistent from year to year as shown by the non-significance of lines x years interaction (Table 1 of the Appendix).

Average days of head of Chinese and Chinese lines with substituted Thatcher, Hope, and Timstein chromosomes in 1953 and 1954 are summarized in Table 6.

On the basis of these data two types of genes, as previously mentioned, are operating. The modifiers on different chromosomes are of unequal effect. Thatcher, Hope, and Timstein possess 10, 10, and 12 of these respectively. Thatcher apparently carries winter growth habit genes on chromosomes XIII and XVIII, Hope and Timstein possess summer growth habit genes on these chromosomes.

Table 3

DAYS TO HEAD OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1952	1953	1954	1954	Average
Chinese	69.00	66.25	65.00	67.50	66.93
Thatcher	63.00	61.00	54.00	58.70	59.18
1	64.25	63.00	57.50	61.80	61.64
2	66.00	64.00	58.50	62.50	62.75
3	64.00	63.00	57.00	62.00	61.50
4	68.00	66.25	63.50	68.10	66.46
5	66.00	64.00	59.00	62.80	62.95
6	64.75	63.00	57.00	62.50	61.81
7	66.00	63.75	58.50	63.30	62.88
8	65.25	63.50	58.00	62.00	62.18
9	64.00	63.00	61.00	66.80	63.70
10	66.00	66.00	62.50	67.30	65.45
11	68.75	66.75	65.00	67.70	67.05
12	64.25	63.00	57.00	61.70	61.48
13		77.75	90.00	88.00	85.25
15	66.00	65.50	63.50	66.00	65.25
16	72.00	66.25	64.00	66.50	67.18
18		83.00	90.00	88.00	87.00
19	68.00	66.75	62.50	66.50	65.94
20	66.25	64.00	60.50	65.50	65.93
21	68.50	66.00	62.50	65.30	65.58
L.S.D. - 5% level	0.42	0.52	1.36	0.48	1.61
1% level	0.57	0.69	1.85	0.76	2.14

Table 4

DAYS TO HEAD OF HOPE, CHINESE, AND CHINESE LINES WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1953	1954	1954	Average
Hope	* 67.00	55.00	62.00	61.33
Chinese	66.75	65.25	67.00	66.33
1	66.50	63.75	66.10	65.45
2	64.25	55.00	62.00	60.41
3	62.25	53.75	61.80	59.27
4	64.75	59.00	62.50	62.08
5	64.50	58.25	62.30	61.68
6	64.50	61.00	65.00	63.50
7	60.00	50.00	59.80	56.60
8	65.25	63.75	66.00	65.00
9	62.25	53.00	62.00	59.08
10	62.25	53.50	61.80	59.18
11	66.75	63.00	67.10	65.61
12	63.75	55.50	62.10	60.45
15	65.50	61.75	66.80	64.68
16	66.50	62.75	67.10	65.45
17	66.25	61.75	66.10	64.70
18		58.50	61.70	60.10
19	* 73.00	64.75	67.00	68.25
20	65.00	65.00	66.70	65.56
21	63.75	55.25	61.70	60.23

* germinated approximately 8 days later than other lines

L.S.D. - 5% level	1.77	1.75	1.61	4.07
1% level	2.25	2.20	1.95	5.44

Table 5

DAYS TO HEAD OF TIMSTEIN, CHINESE, AND CHINESE LINES WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1953	1954	1954	Average
Timstein	60.00	51.00	56.80	55.93
Chinese	66.25	65.25	67.30	66.27
1	65.75	65.00	67.10	65.95
2	66.50	60.00	64.50	63.67
3	64.50	62.00	66.60	64.37
4	65.50	63.50	66.50	65.17
5	64.50	60.75	63.00	62.75
6	63.25	61.25	63.10	62.53
7	65.25	62.75	66.10	64.70
8	64.00	60.25	62.10	62.12
9	68.25	62.00	65.10	65.11
10	* 70.00	62.25	65.80	66.02
11	66.00	63.00	67.30	65.43
12	62.75	59.50	62.00	61.42
15	67.25	64.75	67.10	66.37
16	66.25	66.00	67.10	66.45
17	65.00	63.00	65.60	64.53
18	65.25	61.25	62.60	63.03
19	65.50	63.25	66.00	64.92
20	63.50	62.25	64.50	63.42
21	67.00	65.75	67.10	66.61

* germinated approximately 5 days later than other lines

L.S.D. - 5% level	0.98	1.02	1.16	1.09
1% level	1.31	1.36	1.54	2.88

Table 6

AVERAGE DAYS TO HEAD OF CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER, HOPE, AND TIMSTEIN CHROMOSOMES IN 1953 AND 1954

Chrom.	THATCHER			HOPE			TIMSTEIN			THAT-		TIMS-	
tested	1953	1954[1]	1954[2]	1953	1954[1]	1954[2]	1953	1954[1]	1954[2]	CHER	HOPE	TEIN	LINES
Chinese	66.0	65.0	68.0	67.0	65.0	67.0	66.0	65.0	67.5	66.3	66.3	66.2	66.3
1	63.0	62.5	62.0	66.5	63.5	66.0	66.0	65.0	67.5	62.5	65.3	66.2	64.7
2	64.0	58.5	63.5	64.0	55.0	62.0	67.5	61.0	64.5	62.0	60.3	64.3	62.2
3	63.0	57.0	62.0	62.0	53.5	61.5	64.5	62.5	66.5	60.7	59.0	64.4	61.4
4	66.5	63.5	68.5	65.5	58.5	63.0	65.5	63.5	66.5	66.2	62.3	65.1	64.6
5	64.0	59.0	63.0	64.5	58.0	62.5	63.5	61.0	63.0	62.0	61.7	62.5	62.1
6	63.0	57.0	62.5	64.0	61.0	65.0	63.5	61.0	62.0	60.8	63.3	62.1	62.1
7	63.5	58.5	64.0	60.0	50.0	59.5	65.0	62.5	67.0	62.0	56.5	64.8	61.1
8	63.0	58.0	63.0	65.0	63.5	66.0	64.0	61.0	61.5	61.3	64.8	62.1	62.8
9	63.0	61.0	67.5	62.0	53.0	62.0	68.0	62.5	64.5	63.8	59.0	65.0	62.7
10	66.0	62.5	68.0	62.0	53.0	61.5	70.0	62.0	66.0	65.5	58.9	66.0	63.4
11	66.5	65.0	68.0	67.5	62.5	67.0	66.0	62.5	67.0	66.5	65.7	65.1	65.8
12	63.0	57.0	62.0	63.5	55.5	63.0	63.0	60.0	62.0	60.7	60.7	61.7	61.0
15	66.0	63.5	66.5	66.0	61.5	67.0	67.0	64.5	67.5	65.3	64.8	66.3	65.5
16	66.0	64.0	66.0	66.5	63.0	67.5	66.0	66.0	67.5	65.3	65.7	66.5	65.9
19	66.5	62.5	67.0	73.0	64.5	67.0	65.5	63.5	66.0	65.3	68.2	65.0	66.2
20	64.0	60.5	66.0	65.0	64.5	66.5	63.5	62.5	64.5	63.5	65.3	63.5	64.1
21	66.0	62.5	66.0	64.0	55.5	61.5	67.0	65.5	67.0	64.8	60.3	66.5	63.9
L.S.D. - 5% level --				1.33						--	2.00		-- 3.31
1% level --				1.75						--	2.65		-- 4.45

3. Plant Height

Data on plant height for each set of substitution lines are summarized in Tables 7, 8, and 9.

Plant heights of individual lines were consistent from year to year as shown by the non-significance of the lines x years interaction (Table 14 of the Appendix). It may, therefore, be assumed that differences among substitution lines are largely genetical.

Assuming that differences in plant height exceeding the 5% level of significance are caused by genetic effects of substituted chromosomes three phenotypic classes may be assumed:

(a) height significantly greater than Chinese,

(b) height the same as or similar to Chinese; and

(c) height significantly less than Chinese.

	Significantly greater than Chinese	Same of similar to Chinese	Significantly less than Chinese
Thatcher	XI	I, II, III, IV, V, VII, IX, X, XII, XIII, XV, XVIII, XIX, XX, XXI.	VIII, XVI
Hope		II, IV, V, VI, X, XI, XV, XVI, XVII, XIX, XX, XXI.	I, III, VII, VIII, IX, XII.
Timstein		I, II, III, IV, V, VI, VII, IX, X, XI, XII, XV, XVI, XVII, XVIII, XIX, XX, XXI.	VIII

Only line Chinese XI Thatcher was significantly taller than Chinese. It appears that in Thatcher this chromosome carries the strongest

height increasing genes. Some of the other chromosomes may also have the same or similar effects as chromosome XI only that the corresponding homologues in Chinese carry the same alleles and therefore height is unaltered.

In the group of chromosomes that are the same as or similar to Chinese in height, it is quite likely there either are no effective genes for this character in these chromosomes, or if there are, they have similar effects.

Since the donor varieties Timstein, Thatcher, and Hope are shorter than Chinese on the average by 9.15, 2.52, and 0.3 centimeters respectively, the majority of the lines deviating significantly from Chinese should be shorter. The results conform to expectations. Chinese lines possessing chromosome VIII from all 3 donor varieties were significantly shorter than Chinese. Other lines similar in effect to chromosome VIII were: Chinese XVI Thatcher, Chinese I Hope, Chinese III Hope, Chinese VII Hope, Chinese IX Hope, and Chinese XII Hope. The genetic effects of these chromosomes appear to be the same or similar as shown when lines are compared using the respective L.S.D.'s.

Significant height transgression beyond the limits of both parents was observed in the Thatcher set and beyond Hope, the shorter parent, in the Hope set of substitution lines.

That some homologous chromosomes of the donor varieties have different genetic effects is substantiated by the significant lines x varieties interaction within years as shown in Tables 15 and 16 of the Appendix. The chromosomes having different effects are III, V, VI, VII, IX, X, XII, and XVIII. Taking chromosome XII as an example, we see that Chinese XII Hope is 41.9 inches tall, Chinese XII Thatcher is 50.0 inches tall, and Chinese XII Timstein is 42.3 inches tall. If the

chromosomal effect is due to one gene then there appears to be a multiple allelic series operating for each of the genes on the above chromosomes and these account for the highly significant differences among Chinese lines possessing homologous chromosomes from different donor varieties. Therefore, whether a chromosome from a particular variety will increase or decrease height will depend on the particular allele it carries in relation to the one present in Chinese. However, if the effect of a chromosome is due to more than one gene and a multiple allelic series exists for each, then the problem of determining the number of genes acting becomes extremely complicated.

Data on average plant heights of Chinese and Chinese lines with substituted Thatcher, Hope, and Timstein chromosomes in 1953 and 1954, together with L.S.D.'s for (a) lines within sets within years, (b) lines within sets, and (c) lines over sets and years, are given in Table 10.

It seems clear from the data that some chromosomes have major and others minor genetic effects. A multiple allelic series appears to exist, or else is simulated by combinations of two or more genes, for some of the chromosomes. In any event, eight chromosomes affected plant height significantly; chromosome XI of Thatcher was associated with significant height increase and chromosomes I, III, VII, IX, XII of Hope, XVI of Thatcher and VIII of all 3 donor varieties with significant height decreases. Therefore, at least eight genes or groups of genes affect this quantitative character.

Table 7

PLANT HEIGHT OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1952	1953	1954	Average
Thatcher	44.00	39.80	42.50	42.10
Chinese	43.75	41.00	49.10	44.62
1	45.00	40.90	48.70	44.87
2	43.25	40.30	48.40	43.98
3	45.00	41.70	50.00	45.57
4	43.75	40.10	49.20	44.35
5	43.50	40.60	47.80	43.97
6	44.75	42.70	52.30	46.58
7	43.25	40.20	46.80	43.42
8	40.25	38.80	44.90	41.32
9	41.75	40.90	50.20	44.28
10	43.50	40.70	49.80	44.67
11	45.75	42.00	52.70	46.82
12	44.25	42.40	50.00	45.55
13		41.20	49.90	45.55
15	43.75	41.40	49.40	44.85
16	39.50	40.30	48.00	42.60
17	45.50	41.30		43.40
18		41.80	49.30	45.55
19	44.25	41.40	50.90	45.52
20	43.25	40.70	49.40	44.45
21	42.50	41.00	50.00	44.50
L.S.D. - 5% level	1.09	1.40	4.97	2.06
1% level	1.44	1.87	6.74	2.77

Table 8

PLANT HEIGHT OF HOPE, CHINESE, AND CHINESE LINES
WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1953	1954	Average
Hope	42.7	47.1	44.90
Chinese	41.1	49.3	45.20
1	42.3	50.0	41.15
2	41.0	46.7	43.85
3	40.0	44.6	42.30
4	41.4	48.4	44.90
5	40.6	47.1	43.85
6	40.9	48.4	44.65
7	39.6	43.3	41.45
8	39.4	43.5	41.45
9	38.7	43.3	41.00
10	41.1	46.0	43.55
11	40.5	49.2	44.85
12	41.2	43.4	42.30
15	40.1	47.4	43.75
16	41.7	50.6	46.15
17	40.9	49.2	45.05
18		50.3	50.30
19	42.5	50.1	46.30
20	41.6	49.9	45.75
21	42.5	49.5	46.00
L.S.D. - 5% level	1.37	4.86	2.87
1% level	1.82	6.46	3.92

Table 9

PLANT HEIGHT OF TIMSTEIN, CHINESE, AND CHINESE LINES WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1953	1954	Average
Timstein	36.2	35.4	35.80
Chinese	41.2	48.7	44.95
1	41.5	50.3	45.90
2	41.5	49.3	45.40
3	40.3	48.1	44.20
4	40.4	49.8	45.10
5	43.2	50.4	46.80
6	41.3	47.8	44.55
7	41.3	48.5	44.90
8	38.5	44.9	41.70
9	41.8	47.5	44.65
10	40.8	48.7	44.75
11	42.4	50.6	46.50
12	40.4	47.6	44.00
15	40.1	48.1	44.10
16	40.5	49.2	44.85
17	40.8	50.5	45.65
18	40.7	47.9	44.30
19	43.4	50.5	46.95
20	39.6	46.7	43.15
21	43.1	50.6	46.85
L.S.D. - 5% level	1.76	4.68	3.07
1% level	2.34	6.22	4.18

Table 10

AVERAGE PLANT HEIGHT OF CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER, HOPE, AND TIMSTEIN CHROMOSOMES IN 1953 AND 1954

Chromosome tested	THATCHER 1953	THATCHER 1954	HOPE 1953	HOPE 1954	TIMSTEIN 1953	TIMSTEIN 1954	THATCHER	HOPE	TIMSTEIN	LINES
Chinese	40.9	49.1	40.9	49.7	41.0	48.3	45.0	45.3	44.6	45.0
1	41.2	48.7	42.1	50.2	42.4	50.1	44.9	46.2	46.3	45.8
2	38.6	48.4	41.7	47.2	41.2	47.9	43.5	44.5	44.6	44.2
3	41.8	50.0	40.3	44.7	40.7	48.9	45.9	42.5	44.8	44.4
4	40.5	49.2	41.3	48.4	40.5	48.6	44.8	44.9	44.5	44.7
5	39.3	47.8	40.9	47.0	44.0	49.5	43.5	43.9	46.7	44.7
6	42.4	53.2	40.6	48.5	41.4	47.4	47.8	44.5	44.4	45.6
7	40.2	41.8	39.3	43.1	41.2	48.6	43.5	41.2	44.8	43.2
8	39.0	44.9	39.5	43.8	39.3	45.1	42.0	41.6	42.2	41.9
9	39.5	50.2	39.8	43.4	42.3	47.3	44.9	41.6	44.8	43.7
10	40.4	49.8	41.1	46.3	42.0	44.0	45.1	43.7	45.5	44.8
11	40.8	52.7	40.4	49.9	42.8	51.2	46.7	45.2	47.0	46.3
12	42.4	50.0	41.0	41.9	41.5	46.3	46.2	41.5	43.9	43.8
15	41.2	49.4	39.9	47.4	40.6	47.3	45.3	43.6	44.0	44.3
16	40.1	47.5	41.9	49.7	40.5	49.1	44.0	45.8	44.8	44.9
19	41.5	50.9	41.4	48.5	44.3	50.0	46.2	44.9	47.1	46.1
20	40.8	49.4	40.9	49.7	39.6	47.5	45.1	45.3	43.5	44.6
21	41.0	49.5	42.7	48.4	44.1	49.9	45.2	45.5	47.0	45.9
L.S.D. - 5% level	- 2.24							- 2.03		- 1.95
1% level	- 2.97							- 2.73		- 2.62

4. Lodging

Data on lodging in each of the three sets of Chinese substitution lines are summarized in Tables 11, 12, and 13.

The donor varieties have much greater lodging resistance than the recipient parent. If lodging is genetically controlled, some of the substitution lines possessing chromosomes from the more lodging resistant donor varieties should show less susceptibility to lodging than Chinese. Also, some of the substitution lines might have less lodging resistance than Chinese. If the differences among the lines were largely environmental and not genetical, little or no consistency would be expected in line-lodging-values from year to year. Lodging scores for most individual lines were, however, very consistent, as shown by the non-significance of the lines x years interaction (Table 24 of the Appendix). It can be assumed, therefore, that differences among substitution lines were caused by genetic differences affecting this character. A few lines, however, were not consistent. They are Chinese XVI Thatcher, Chinese XIX Thatcher, Chinese II Hope, Chinese XIX Hope, and Chinese IX Timstein. It was mainly because of this inconsistency of lines within sets that caused the triple interaction lines x years x varieties to be significant. The interaction is, however, difficult to interpret.

Assuming that differences in lodging resistance exceeding the 5% level of significance are caused by genetic effects of substituted chromosomes three phenotypic classes may be assumed:

(a) lodging resistance significantly greater than Chinese,

(b) lodging resistance the same as or similar to Chinese, and

(c) lodging resistance significantly less than Chinese.

	Thatcher set of substitution lines.	Hope set of substitution lines.	Timstein set of substitution lines.
Significantly greater than Chinese	I, II, III, IV, V, VI, VII, VIII, IX, XII, XIII, XVI, XIX, XX, XXI.	I, II, III, IV, V, VI, VII, VIII, IX, XII, XVII, XIX, XXI.	I, IV, V, VIII, IX, X, XV, XVIII, XIX.
Similar to Chinese	X, XI, XV, XVIII.	X, XI, XV, XVI, XVIII, XX.	II, III, VI, VII, XI, XVI, XVII, XX, XXI.
Significantly less than Chinese	-----	-----	-----

None of the lines were significantly lower in lodging than Chinese.

In the group of chromosome lines that are not significantly different from Chinese, it is very likely that there are either no effective genes for this character on these chromosomes of both the donor and recipient varieties, or if there are, they have similar effects.

The group of lines that are significantly stronger strawed than Chinese is rather large, and varies with the different donor parents. One of the main reasons for the large number of significant lines is that Chinese is a very weak strawed variety and the donors are very strong strawed. The effects of the chromosomes that give significant results are not all equal. Some of the lines significantly higher than Chinese are significantly higher or lower than other lines showing significant results. Chinese I Thatcher, for example, is significantly more resistant to lodging than Chinese XXI Thatcher, yet both are significantly more resistant to lodging than Chinese. This indicates that some chromo-

somes have major and others minor genetic effects.

The interaction lines x varieties within years (Tables 25 and 26 of the Appendix) was highly significant. This may be interpreted to mean that some of the homologous chromosomes of donor and recipient varieties are significantly different in genetic effects from each other. Chromosome XXI is of this type. Chinese XXI Thatcher and Chinese XXI Hope were resistant and Chinese XXI Timstein was susceptible. Other chromosome lines showing the same type of effect are I, IV, VII, X, XIX, and XX.

Table 14 shows the average lodging scores of Chinese and Chinese lines with substituted Thatcher, Hope, and Timstein chromosomes in 1953 and 1954. L.S.D.'s were computed for (a) lines within sets within years, (b) lines within sets, and (c) lines over sets and years.

If the line effect is due to one gene per chromosome, lines which are non-significantly different from Chinese may be assumed to possess the same allele as the recipient parent. An alternative to this is possible. Since lodging is probably controlled by many genes and since each gene has a very small effect, (even though certain lines are statistically non-significantly different from Chinese) the chromosome from the donor variety may carry a different allele. If the assumption that each chromosome affects lodging through the action of a single gene is correct, and since homologous chromosome lines vary in lodging resistance, we must assume a series of multiple alleles of different strengths affecting lodging. Statistical substantiation for this assumption is present in Tables 25 and 26 of the Appendix.

The alternative to the above situation may be that the effect of any one chromosome is due to more than one gene with or without a series of alleles for each. If the chromosomes effect is dependent on the

number of genes present, with genes on all chromosomes having equal or approximately equal effects, then line differences are rough estimations of number of genes. However, if chromosomes differ in number of genes and a multiple allelic series exists for each gene, a very complex organization of almost impossible genetic determination exists. In any event, it is clear from the data that there are some chromosomes that have what may be termed major genetic effects as well as those having minor genetic effects.

Since none of the lines were significantly lower in lodging resistance than Chinese, it is possible that Chinese possesses most of the genes for low lodging resistance. Also, the donors appear to possess a near maximum of resistance genes. Since many chromosomes affect lodging significantly, 15 in Thatcher, 13 in Hope and 10 in Timstein, it seems that the effects of individual genes are small, although not necessarily equal as previously shown. From these studies, it appears that lodging is a genetically complex character affected by at least 15 genes or groups of genes.

Table 11

LODGING SCORES OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1952*	1953*	1954*	Average
Thatcher	10.0	9.6	9.8	9.8
Chinese	4.5	4.0	3.5	4.0
1	9.0	8.2	8.5	8.6
2	8.0	7.0	7.5	7.5
3	7.0	6.3	5.8	6.4
4	6.0	5.5	6.0	5.8
5	7.0	7.7	8.5	7.7
6	7.0	6.0	6.5	6.5
7	7.0	6.3	6.8	6.7
8	8.5	8.0	7.8	8.1
9	8.0	7.8	6.5	7.4
10	5.5	4.4	2.5	4.1
11	4.5	4.2	3.8	4.2
12	6.0	6.1	5.5	5.9
13	7.0	6.2		6.6
15	5.5	3.9	4.0	4.5
16	6.0	6.6	4.0	5.5
18		4.6		4.6
19	6.0	4.6	6.5	5.7
20	6.0	6.0	6.5	6.2
21	6.5	6.5	7.0	6.7
L.S.D. - 5% level	1.19	1.19	3.58	1.05
1% level	1.58	1.58	4.86	1.41

* 1952, 1953 - 4 replicates

* 1954 - 2 replicates

Table 12

LODGING SCORES OF HOPE, CHINESE, AND CHINESE LINES
WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1953	1954	Average
Hope	9.1	9.6	9.4
Chinese	4.4	3.5	4.0
1	6.8	6.0	6.4
2	7.1	8.3	7.7
3	7.5	7.6	7.6
4	6.6	5.3	6.0
5	7.0	7.1	7.1
6	6.2	6.8	6.5
7	7.1	8.3	7.7
8	7.4	6.4	6.9
9	7.3	8.5	7.9
10	5.5	5.3	5.4
11	3.4	2.6	3.0
12	7.1	7.5	7.3
15	4.4	4.8	4.6
16	5.0	4.9	5.0
17	5.5	6.9	6.2
18		5.0	5.0
19	7.9	4.6	6.3
20	4.7	2.6	3.7
21	6.6	8.3	7.5
L.S.D. - 5% level	2.34	3.58	1.86
1% level	3.12	4.76	2.55

Table 13

LODGING SCORES OF TIMSTEIN, CHINESE, AND CHINESE LINES WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1953	1954	Average
Timstein	9.3	10.0	9.7
Chinese	5.2	3.5	4.4
1	7.1	6.9	7.0
2	5.6	6.8	6.2
3	5.6	5.1	5.4
4	6.6	6.4	6.5
5	7.4	8.4	7.9
6	5.9	6.1	6.0
7	5.7	5.9	5.8
8	8.6	7.6	8.1
9	4.7	8.5	8.0
10	8.4	7.3	7.9
11	5.4	5.5	5.5
12	5.5	7.0	6.3
15	5.7	7.0	6.4
16	5.9	4.9	5.4
17	6.1	6.3	6.2
18	5.9	6.9	6.4
19	8.3	7.5	7.9
20	4.7	3.5	4.1
21	5.2	4.0	4.6
L.S.D. - 5% level	1.32	2.94	1.88
1% level	1.76	3.91	2.56

Table 14

AVERAGE LODGING SCORES OF CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER, HOPE, AND TIMSTEIN CHROMOSOMES IN 1953 AND 1954

Chromosome tested	THATCHER 1953	THATCHER 1954	HOPE 1953	HOPE 1954	TIMSTEIN 1953	TIMSTEIN 1954	THATCHER	HOPE	TIMSTEIN	LINES
Chinese	3.7	3.5	3.9	3.0	4.6	3.5	3.6	3.5	4.1	3.7
1	8.1	8.5	7.4	6.0	6.9	6.3	8.3	6.7	6.6	7.2
2	6.6	7.5	5.9	8.3	5.7	6.5	7.1	7.1	6.1	6.7
3	5.6	5.8	7.3	7.3	4.8	4.8	5.7	7.3	4.8	5.9
4	4.6	3.0	7.0	5.5	6.1	5.8	3.8	6.3	5.9	5.3
5	8.0	8.5	6.3	7.8	8.5	9.0	8.3	7.0	8.8	8.0
6	6.1	6.5	5.9	6.5	5.5	6.3	6.3	6.2	5.9	6.1
7	6.4	6.8	8.3	8.3	5.3	5.8	6.6	8.3	5.5	6.8
8	8.1	7.8	7.0	6.8	8.4	7.3	7.9	6.9	7.8	7.5
9	8.6	6.5	7.2	8.5	4.7	8.3	7.6	7.9	6.5	7.3
10	3.6	2.5	4.6	5.0	8.3	7.5	3.1	4.8	7.9	5.3
11	4.1	3.8	3.3	2.3	4.8	5.0	3.9	2.8	4.9	3.9
12	6.4	5.5	7.0	7.0	5.4	7.0	6.0	7.0	6.2	6.4
15	3.7	4.0	3.5	5.0	5.2	6.8	3.9	4.3	6.0	4.7
16	7.4	4.0	4.1	4.8	4.5	5.3	5.7	4.4	4.9	5.0
19	3.7	6.5	7.6	4.3	8.2	7.0	5.1	5.9	7.6	6.2
20	6.5	6.5	4.2	2.3	3.6	3.0	6.5	3.2	3.3	4.3
21	6.2	7.0	7.0	8.3	5.3	3.5	6.6	7.6	4.4	6.2
L.S.D. - 5% level		--	1.63					1.99		2.02
1% level		--	2.15					2.67		2.72

* Two replicates from each set of substitution lines were used to compute above values.

5. Protein Content

Data on protein content of Thatcher, Chinese, and Chinese lines with substituted Thatcher chromosomes are summarized in Table 15.

Although protein content is greatly influenced by environmental conditions, most of the chromosome lines gave consistent results from year to year.

Lines V, VII, IX, XV, and XVI were significantly higher in protein content, at the 5% level, than Chinese. These lines also transgressed the protein content of the donor variety. None of the 19 lines tested were significantly lower in protein content than Chinese.

Inheritance of protein content in this set of substitution lines appears to be controlled by genes on at least five chromosomes, V, VII, IX, XV, and XVI. Whether the chromosomal effect is due to one or more genes cannot be determined at present. However, the effects of genes on different chromosomes, whose lines are significantly different from Chinese, appear to be similar (Table 15). In cases where lines are not significantly different from Chinese two assumptions may be made. Homologous chromosomes of both donor and recipient varieties carry similar or nearly similar genes or they do not carry any genes affecting this character.

Table 15

PROTEIN CONTENT OF THATCHER, CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1950	1951	1952	1953	Average
1	16.5	12.4	14.2	13.4	14.1
2	16.6	13.2	14.1	14.8	14.7
3	16.6	13.0	13.7	14.4	14.4
4	16.3	13.2	13.7	15.0	14.6
5	17.2	14.6	13.7	15.7	15.3
6	15.9	13.2	13.6	15.0	14.4
7	16.7	14.2	14.4	15.4	15.2
8	16.3	12.9	13.8	14.2	14.3
9	16.4	14.8	14.1	14.9	15.1
10	15.4	13.6	14.1	15.0	14.5
11	16.5	13.2	13.7	15.4	14.7
12	15.9	12.8	13.3	14.3	14.1
13			13.8	14.4	14.1
15	16.1	14.1	14.1	15.2	14.9
16	17.3	14.3	14.7	14.9	15.3
18	15.7	14.0	13.8	14.5	14.5
19	16.1	12.7	13.3	14.4	14.1
20	16.5	13.4	13.9	14.8	14.7
21	16.1	13.9	14.2	15.0	14.8
Thatcher	16.6	13.7	14.1	15.2	14.9
Chinese	15.7	12.8	13.4	14.7	14.2

L.S.D. --	5% level	0.60
	1% level	0.80

6. Spike Density

Data on spike density for each of the three sets of Chinese substitution lines are summarized in Tables 16, 17, and 18.

No major gene differences for spike density have been found by conventional methods between varieties within the *vulgare* species possessing lax spikes. Since the donor and recipient varieties are all lax spiked no major gene differences should be expected in the substitution lines. Varieties within the *vulgare* species probably differ only in number of minor genes distributed on the various chromosomes.

The donor varieties were in all cases less dense than the recipient variety. None of the lines were as lax as the donor varieties. Most of the lines had densities equal to or lower than Chinese. Spike densities of individual lines were consistent from year to year as was shown by the non significance of the lines x years interaction (Table 34 of the Appendix). Chinese XVI Thatcher showed the most marked deviation; in 1952, it was highly significant, and in 1953 and 1954 it was equal to Chinese in spike density.

As expected, results indicate no major gene differences; only minor genes modifying the degree of density were presumably associated with specific chromosomes.

If differences in spike density exceeding the 5% level are those caused by genetic effects of substituted chromosomes, then the following three phenotypic classes may be assumed: (1) those significantly more dense than Chinese, (11) those the same as or similar to Chinese, and (111) those significantly less dense than Chinese.

	Thatcher	Hope	Timstein
Significantly more dense	IV	II	XII
Same as or similar to Chinese	II, V, VI, XI, XII, XIII, XV, XVI, XVIII, XX	I, III, IV, V, VI, VII, IX, XI, XII, XV, XVI, XVII, XVIII, XIX, XXI	I, II, IV, IX, XV, XVII, XVIII
Significantly less dense	I, III, VI, VIII, IX, X, XIX, XXI	VIII, X, XX	III, V, VI, VII, VIII, X, XI, XVI, XIX, XX, XXI

Three lines, Chinese IV Thatcher, Chinese II Hope, and Chinese XII Timstein transgressed the density of Chinese by being significantly more dense. Thatcher chromosome IV seems to carry genes decreasing spike length, the number of spikelets remaining the same as in Chinese. In Hope chromosome II and Timstein chromosome XII both spike length and spikelet number are disproportionally decreased.

In the group of chromosomes that are not significantly different from Chinese, it is quite likely that either there are no effective genes for this character on these chromosomes of both the donor and recipient varieties, or if there are, they have similar effects. Substitution lines XV and XVIII of all 3 donor varieties were similar to the recipient parent in spike density.

Thatcher chromosomes I, III, VI, VIII, IX, X, XIX, and XXI; Hope chromosomes VIII, X, and XX, and Timstein chromosomes III, V, VI, VII, VIII, X, XI, XVI, XIX, XX, and XXI produce lines with significantly less spike density than Chinese. Substitution lines Chinese X Thatcher, Chinese VIII of Hope, Chinese XX Hope and Chinese XX Timstein had spike

density values 0.5 to 0.7 centimeters lower than Chinese. The other lines did not show as striking results. The fact that different chromosomes within each set of substitution lines gave significantly more dense types, similar types, and significantly less dense types, than Chinese shows that the effects of the chromosomes are not equal. This seems to signify that some chromosomes have major and others minor genetic effects. Also, there probably are chromosomes with no effect on this character. Generally, results seem to show that both strong and weak minor genes are present on different chromosomes within a variety. The degree to which any variety will be more or less dense than any other will depend on the number of accumulated strong and weak minor genes.

Since we are testing whole chromosomes it is impossible on this basis to predict whether the chromosome behavior with respect to spike density is due to one or more genes. That homologous chromosomes from different varieties are, in some cases, significantly different in genetic effects from each other is substantiated by a highly significant lines x variety interaction (Tables 35 and 36 of the Appendix). This significant interaction may support either of three alternatives: (a) individual chromosomes affect spike density due to one gene per chromosome with a series of 2 or more alleles, or (b) each chromosome may possess more than one gene and each of these may possess a series of 2 or more alleles, and (c) a mixture of both.

Average spike densities of Chinese and Chinese lines with substituted Thatcher, Hope, and Timstein chromosomes in 1953 and 1954 are summarized in Table 19 together with L.S.D.'s for (a) lines within years within sets, (b) lines within sets, and (c) lines over years and sets.

Chromosomes with major and minor effects modify spike density. Some chromosomes as IV of Thatcher, II of Hope, and XII of Timstein all

increase density significantly and to the same degree. Eight chromosomes of Thatcher, three of Hope, and eleven of Timstein decrease density significantly; the degree of spike density varies with different chromosomes.

Table 16

SPIKE DENSITIES OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1952	1953	1954	Average
Thatcher	2.36	1.96	2.31	2.21
Chinese	3.26	2.88	3.47	3.20
1	2.90	2.70	3.13	2.91
2	3.18	2.71	3.27	3.05
3	2.99	2.34	2.98	2.77
4	3.73	3.07	3.61	3.47
5	3.17	2.69	3.10	2.99
6	2.98	2.38	3.04	2.80
7	3.36	2.63	3.13	3.04
8	3.39	2.30	2.81	2.83
9	2.90	2.52	2.94	2.79
10	2.94	2.38	2.74	2.69
11	3.12	2.78	3.33	3.08
12	3.24	2.50	3.09	2.94
13		2.99	3.22	3.11
15	3.46	2.66	3.41	3.18
16	4.23	2.80	3.44	3.49
18		3.14	3.36	3.25
19	3.10	2.60	3.02	2.91
20	3.35	2.53	3.28	3.05
21	2.86	2.54	2.93	2.78
L.S.D. - 5% level	0.149	0.088	0.236	0.27
1% level	0.198	0.117	0.320	0.37

Table 17

SPIKE DENSITIES OF HOPE, CHINESE, AND CHINESE LINES WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1953	1954	Average
Hope	1.96	2.33	2.15
Chinese	2.93	3.33	3.13
1	2.95	3.28	3.12
2	3.28	3.75	3.52
3	2.79	3.28	3.04
4	2.86	3.33	3.10
5	2.73	3.23	2.98
6	2.63	3.13	2.88
7	2.71	3.27	2.99
8	2.41	2.88	2.65
9	3.08	3.64	3.36
10	2.22	2.74	2.48
11	2.89	3.17	3.03
12	3.21	3.56	3.39
15	2.84	3.23	3.04
16	3.00	3.48	3.24
17	2.65	3.18	2.92
18		3.40	3.40
19	2.86	3.19	3.03
20	2.33	3.01	2.67
21	2.72	3.23	2.98
L.S.D. - 5% level	0.100	0.184	0.33
1% level	0.133	0.245	0.46

Table 18

SPIKE DENSITIES OF TIMSTEIN, CHINESE, AND CHINESE LINES
WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1953	1954	Average
Timstein	1.76	2.05	1.91
Chinese	2.91	3.44	3.18
1	2.82	3.30	3.06
2	2.96	3.63	3.30
3	2.54	3.04	2.79
4	2.97	3.63	3.30
5	2.66	3.18	2.92
6	2.64	3.22	2.93
7	2.69	3.28	2.99
8	2.63	3.22	2.93
9	2.84	3.65	3.25
10	2.74	3.09	2.92
11	2.65	3.06	2.86
12	3.18	3.68	3.43
15	3.07	3.37	3.22
16	2.69	3.30	3.00
17	2.75	3.39	3.07
18	2.93	3.51	3.22
19	2.70	3.15	2.93
20	2.19	2.76	2.48
21	2.72	3.24	2.98
L.S.D. - 5% level	0.092	0.130	0.18
1% level	0.122	0.173	0.25

Table 19

AVERAGE SPIKE DENSITIES OF CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER, HOPE, AND TIMSTEIN CHROMOSOMES IN 1953 AND 1954

Chromosome tested	THATCHER 1953	THATCHER 1954	HOPE 1953	HOPE 1954	TIMSTEIN 1953	TIMSTEIN 1954	THATCHER	HOPE	TIMSTEIN	LINES
Chinese	2.91	3.47	2.98	3.43	2.86	3.49	3.19	3.20	3.17	38.25
1	2.73	3.13	2.96	3.25	2.89	3.29	2.93	3.10	3.09	36.46
2	2.75	3.27	3.24	3.73	2.92	3.64	3.00	3.48	3.28	39.07
3	2.39	2.98	2.82	3.28	2.61	3.04	2.68	3.05	2.82	34.20
4	3.08	3.61	2.85	3.29	3.01	3.64	3.34	3.07	3.32	38.94
5	2.76	3.10	2.76	3.12	2.70	3.23	2.93	2.94	2.96	35.31
6	2.40	3.04	2.64	3.06	2.68	3.21	2.72	2.84	2.94	34.01
7	2.65	3.13	2.71	3.34	2.67	3.38	2.89	3.02	3.02	35.73
8	2.32	2.81	2.45	2.93	2.64	3.16	2.56	2.69	2.89	32.58
9	2.52	2.94	3.14	3.58	2.85	3.72	2.73	3.36	3.28	37.46
10	2.31	2.74	2.24	2.75	2.78	3.07	2.52	2.49	2.92	31.73
11	2.80	3.33	2.90	3.19	2.67	3.11	3.06	3.04	2.89	35.96
12	2.50	3.09	3.20	3.57	3.18	3.81	2.80	3.38	3.49	38.68
15	2.69	3.41	2.86	3.23	3.14	3.43	3.05	3.05	3.28	37.50
16	2.82	3.44	2.99	3.43	2.72	3.27	3.13	3.21	2.99	37.33
19	2.61	3.02	2.90	3.16	2.68	3.14	2.82	3.03	2.91	34.99
20	2.55	3.28	2.30	2.96	2.25	2.75	2.91	2.63	2.50	32.15
21	2.59	2.93	2.78	3.23	2.77	3.21	2.76	3.00	2.99	34.99
L.S.D. - 5% level		--		0.20				--	0.20 --	0.38
1% level		--		0.26				--	0.26 --	0.52

7. Thousand-Kernel Weight

Data on thousand-kernel weight in each of the three sets of Chinese substitution lines are summarized in Tables 20, 21, and 22.

The donor parents, Thatcher, Hope, and Timstein, were each significantly heavier (5% level) in thousand-kernel weight than Chinese. Chinese XVI Thatcher was the only line that was significantly lower in thousand-kernel weight than the recipient variety.

The following lines were significantly heavier (5% level) in thousand-kernel weight than Chinese: Chinese I Thatcher, Chinese V Thatcher, Chinese I Hope, Chinese IV Hope, Chinese VI Hope, Chinese I Timstein, Chinese V Timstein, Chinese VI Timstein, Chinese X Timstein, and Chinese XIX Timstein.

It may be assumed that at least seven chromosomes, I, IV, V, VI, X, XVI, and XIX, carry genes affecting kernel weight. Chromosome I had the greatest effects involving all three donor varieties. In every case the size of kernel was significantly increased by the substitution of this chromosome. Chinese XVI Thatcher line showed a significant reduction in kernel size.

Table 20

THOUSAND-KERNEL WEIGHTS OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1953	1953	1954	Average
Thatcher	30.9	32.4	30.7	31.3
Chinese	27.0	22.6	18.6	22.7
1	30.3	32.1	26.4	29.6
2	27.6	25.5	19.8	24.3
3	27.3	24.1	21.7	24.4
4	26.9	24.3	16.8	22.7
5	28.7	24.5	23.5	25.6
6	27.7	21.8	23.7	24.4
7	27.3	22.4	20.5	23.4
8	28.5	25.9	17.9	24.1
9	27.9	23.3	18.2	23.1
10	24.2	21.8	17.4	21.1
11	28.7	22.1	18.2	23.0
12	27.5	24.1	17.7	23.1
13		24.0	21.4	22.7
15	24.8	21.6	19.6	22.0
16	19.9	21.0	17.0	19.3
18	22.6	22.2	16.1	20.3
19	25.3	24.6	19.9	23.3
20	26.7	22.9	17.2	22.3
21	26.2	25.8	19.5	23.8
L.S.D. - 5% level				3.00
1% level				4.00

Table 21

THOUSAND-KERNEL WEIGHTS OF HOPE, CHINESE, AND CHINESE LINES WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1952	1953	1954	Average
Hope	34.2	38.7	36.7	36.5
Chinese	26.7	22.2	18.8	22.6
1	28.0	29.4	23.6	27.0
2	25.0	26.1	23.2	24.8
3	27.1	24.0	26.3	25.8
4	28.1	28.5	21.7	26.1
5	27.7	25.5	21.4	24.9
6	29.6	27.0	23.8	26.8
7	25.7	23.1	23.7	24.2
8	23.7	22.8	19.6	22.0
9	27.5	23.7	21.9	24.0
10	24.6	22.8	21.9	23.1
11	23.7	21.9	22.3	22.6
12	27.4	25.8	21.9	25.0
15	26.3	22.5	20.3	23.0
16	24.7	24.3	19.0	22.7
17	28.2	23.5	20.4	24.0
18	20.3	21.9	19.4	20.5
19	25.7	28.2	16.9	23.6
20	27.0	19.8	17.5	21.4
21	26.9	24.3	21.1	24.1
L.S.D. - 5% level				3.3
1% level				4.4

Table 22

THOUSAND-KERNEL WEIGHTS OF TIMSTEIN, CHINESE, AND CHINESE LINES WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1952	1953	1954	Average
Timstein	37.6	31.8	37.4	35.6
Chinese	27.2	22.6	18.6	22.8
1	29.4	29.1	20.8	26.4
2	28.8	23.5	20.7	24.3
3	28.5	22.8	20.0	23.8
4	28.3	25.5	19.4	24.4
5	30.4	25.6	23.6	26.5
6	30.4	24.3	22.6	25.8
7	24.0	21.6	21.4	22.3
8	26.4	26.4	19.8	24.2
9		22.8	20.0	21.6
10	27.4	26.4	21.9	25.2
11	28.4	23.7	19.7	23.9
12	27.6	21.6	20.1	23.1
15	25.3	22.5	16.6	21.5
16	25.5	24.3	20.1	23.3
17	25.6	22.2	20.9	22.9
18	25.9	21.9	20.6	22.8
19	28.3	26.1	22.5	25.6
20	28.4	19.8	18.2	22.1
21	26.9	25.5	20.4	24.3
L.S.D. - 5% level				2.4
1% level				3.2

8. Yield

Data on yield of Thatcher, Hope, and Timstein sets of substitution lines are summarized in Tables 23, 24, and 25 respectively.

Accessory factors affecting yield such as drought, various diseases and insects, variable soil fertility, etc. were either not present or reduced to a minimum. Lodging and other characters such as kernel size, however, varied from line to line and may have affected yield. Despite the presence of some of these factors yields of individual lines were reasonably consistent from year to year as shown by the non-significance of the lines x years interaction (Table 58 of the Appendix).

All three donor varieties outyielded Chinese by 180 to 200%. None of the substitution lines were higher yielding than the critical donor variety, and several were lower (non significantly) than Chinese.

Granting that yield values of substitution lines exceeding the 5% level of significance are caused by genetic effects of transferred chromosomes, then three classes may be assumed: (1) those significantly higher yielding than Chinese, (11) those the same as or similar to Chinese, and (111) those significantly lower yielding than Chinese.

	Thatcher	Hope	Timstein
Significantly higher than Chinese.	I, III, VIII, XII	I, IV, V, VI, VII, VIII, IX, X, XII, XXI	I, II, III, IV, V, VI, VII, VIII, XII, XVI, XVII, XVIII, XIX, XXI
Same as or similar to Chinese.	II, IV, V, VI, VII, IX, X, XI, XIII, XV, XVI, XVIII, XIX, XX, XXI	II, III, XI, XV, XVI, XVII, XVIII, XIX, XX	IX, X, XI, XV, XX

None of the previously stated substitution lines were significantly lower yielding than Chinese.

In the class of chromosome lines that are not significantly different from Chinese, which includes 15 Thatcher, 9 Hope, and 5 Timstein chromosomes, it is quite likely that either there are no effective genes for this character on these chromosomes, or if there are, they have similar effects to genes in Chinese. Chromosomes XI, XV, and XX of all 3 donor varieties were not significantly different from Chinese. These chromosomes probably carry no differential genes affecting this character.

The number of lines that are significantly different varies with the donor varieties. Four Thatcher chromosomes I, III, VIII, and XII, ten Hope chromosomes I, IV, V, VI, VII, VIII, IX, X, XII, and XXI, gave lines significantly higher yielding than Chinese. Chromosome lines I, VIII, and XII of all 3 donor varieties were higher yielding than Chinese. In the set of substitution lines possessing Thatcher chromosomes, line one was the highest yielding (58.6% more than Chinese), however, it was not significantly different from lines three, eight, and twelve. In the Hope set of substitution lines, chromosomes I and XII are significantly higher yielding than chromosome lines, IV, V, VI, VII, VIII, IX, X, and XXI, which are not significantly different from each other. In the Timstein set the effects are still more variable. Chromosome I is significantly different from IV and XIX which in turn are significantly different from II, III, V, VI, VII, XVI, XVII, XVIII, and XXI. The latter group of chromosomes are not significantly different from each other. This signifies that different chromosomes of the same variety affect this character unequally, at times significantly so. In the Thatcher set the significantly different lines yielded 34.6 to 58.6% more than Chinese. Most of the Hope chromosome lines yield 19.7 to 37.0%

more than Chinese only I (45.9%) and XII (46.8%) yield higher. Ten of the fourteen Timstein chromosome lines yield 12 to 20% higher than Chinese while lines I, IV, VIII, and XIX yield 31 to 52% more than Chinese. Thatcher appears to possess a few major genes for yield while Hope and Timstein appear to carry minor genes mainly with only a few major genes. Chinese seems to have an accumulation of a large number of genes that give low yield, presumably recessives of dominant vigour genes.

The interaction, lines x varieties (Tables 59 and 60 of the Appendix), was highly significant and may be interpreted as meaning that some of the homologous chromosomes of different varieties are significantly different from each other in genetic effects. Chromosome XII is of this type. Chinese XII Thatcher yields 37.7% more than Chinese while Chinese XII Hope and Chinese XII Timstein yield 46.8 and 11.8% more, respectively -- a variation of 31% among different homologous chromosome XII lines. Other chromosomes with similar effects are IV, VII, IX, XI, XVI, and XIX.

Average yields of Chinese and Chinese lines with substituted Thatcher, Hope, and Timstein chromosomes are summarized in Table 26 together with L.S.D.'s for (a) lines within years within sets, (b) lines within sets, and (c) lines over years and sets.

On the basis of the results obtained it seems that yield is controlled by numerous genes located on at least 4 chromosomes in Thatcher, 10 in Hope, and 14 in Timstein.

Table 23

YIELDS OF THATCHER, CHINESE, AND CHINESE LINES WITH SUBSTITUTED THATCHER CHROMOSOMES

Chromosome tested	1952	1953	1954	Average
Thatcher	1003.75 (150.5)	1205.00 (220.0)	832.50 (233.4)	1013.75 (193.6)
Chinese	667.00 (100.0)	547.50 (100.0)	356.70 (100.0)	523.73 (100.0)
1	908.75 (136.2)	1017.50 (185.8)	565.80 (158.6)	830.68 (158.6)
2	775.75 (116.3)	777.50 (142.0)	492.50 (138.1)	681.92 (130.2)
3	851.25 (127.6)	752.50 (137.4)	510.80 (143.2)	704.85 (134.6)
4	659.75 (98.9)	587.50 (107.3)	259.20 (72.7)	502.15 (95.8)
5	741.50 (111.2)	792.50 (144.7)	500.80 (140.4)	678.26 (129.5)
6	803.25 (120.4)	575.00 (105.0)	515.80 (144.6)	631.35 (120.5)
7	673.25 (100.9)	725.00 (132.4)	491.70 (137.8)	629.98 (120.3)
8	908.75 (136.2)	860.00 (157.1)	521.70 (146.3)	763.48 (145.8)
9	782.25 (117.3)	777.50 (142.0)	461.70 (129.4)	673.82 (128.7)
10	740.25 (110.3)	682.50 (124.7)	454.20 (127.3)	625.65 (119.5)
11	674.50 (101.1)	522.50 (95.4)	281.70 (79.0)	492.90 (94.1)
12	949.75 (142.4)	732.50 (133.7)	481.70 (135.0)	721.32 (137.7)
13		575.00 (105.0)	*277.50 (77.8)	426.25
15	806.50 (120.9)	532.50 (97.3)	403.30 (113.1)	580.77 (110.9)
16	444.25 (66.7)	567.50 (103.5)	407.50 (114.2)	473.08 (90.3)
18		570.00 (104.1)	*195.80 (54.9)	382.90
19	806.75 (121.0)	650.00 (118.7)	485.80 (136.2)	647.52 (123.6)
20	738.50 (110.7)	600.00 (109.5)	432.50 (121.3)	590.33 (112.7)
21	829.25 (124.3)	727.50 (132.9)	509.20 (142.8)	688.65 (131.5)
L.S.D. 5% level	149.40	66.07	67.39	183.9
1% level	198.90	87.81	89.11	246.7

* harvested when the lines were still green and immature

Values in brackets are yields in percentage of Chinese whose yield is taken as 100%.

Table 24

YIELDS OF HOPE, CHINESE, AND CHINESE LINES WITH SUBSTITUTED HOPE CHROMOSOMES

Chromosome tested	1953		1954		Average	
Hope			675.8	(184.3)		
Chinese	602.5	(100.0)	366.7	(100.0)	484.6	(100.0)
1	875.0	(145.2)	539.2	(147.0)	707.1	(145.9)
2	627.5	(104.2)	476.7	(129.9)	552.1	(113.9)
3	645.0	(107.1)	486.7	(132.7)	565.9	(116.8)
4	662.5	(109.9)	497.5	(135.7)	580.0	(119.7)
5	735.0	(122.0)	499.2	(136.1)	617.1	(127.3)
6	747.5	(124.1)	510.8	(139.3)	629.2	(129.8)
7	807.5	(134.0)	521.7	(142.3)	664.6	(137.1)
8	770.0	(127.8)	505.8	(138.0)	637.9	(131.6)
9	750.0	(124.5)	501.7	(136.8)	625.9	(129.2)
10	727.5	(120.7)	517.5	(141.1)	622.5	(128.5)
11	552.5	(91.7)	371.7	(101.4)	462.1	(95.4)
12	877.5	(145.6)	545.0	(148.6)	711.3	(146.8)
15	625.0	(103.7)	466.7	(127.3)	545.9	(112.7)
16	567.5	(94.2)	379.2	(103.4)	473.4	(97.7)
17	627.5	(104.2)	467.5	(127.5)	547.5	(112.9)
18			445.0	(121.4)		
19	625.0	(103.7)	429.2	(117.0)	527.1	(108.8)
20	602.5	(100.0)	405.0	(113.2)	503.8	(104.0)
21	777.5	(129.0)	534.2	(145.7)	655.9	(135.3)
L.S.D. 5% level	67.87		64.42		82.78	
1% level	90.58		84.92		113.39	

Values in brackets are yields in percentage of Chinese whose yield is taken as 100%.

Table 25

YIELDS OF TIMSTEIN, CHINESE, AND CHINESE LINES WITH SUBSTITUTED TIMSTEIN CHROMOSOMES

Chromosome tested	1953		1954		Average	
Timstein	1087.50	(178.6)	828.33	(231.2)	957.92	(198.1)
Chinese	608.75	(100.0)	358.33	(100.0)	483.54	(100.0)
1	935.00	(153.6)	540.00	(150.7)	737.50	(152.5)
2	620.00	(101.8)	466.67	(130.2)	543.33	(112.4)
3	667.50	(109.7)	442.50	(123.5)	555.00	(114.8)
4	777.50	(127.7)	498.16	(136.5)	633.33	(131.0)
5	647.50	(106.4)	455.83	(127.2)	551.67	(114.1)
6	658.75	(108.2)	469.17	(130.9)	563.96	(116.6)
7	620.00	(101.8)	479.17	(133.7)	549.59	(113.7)
8	867.50	(142.5)	538.33	(150.2)	702.92	(145.4)
9	561.25	(92.2)	405.83	(113.3)	483.54	(100.0)
10	428.75	(70.4)	421.67	(117.7)	425.21	(87.9)
11	618.75	(101.6)	392.50	(109.5)	505.63	(104.6)
12	661.25	(108.6)	458.33	(127.9)	559.79	(115.8)
15	617.50	(101.4)	356.67	(99.5)	487.09	(100.7)
16	690.00	(113.3)	474.17	(132.3)	582.09	(120.4)
17	642.50	(105.5)	448.33	(125.1)	545.42	(112.8)
18	637.50	(104.7)	465.83	(130.0)	551.67	(114.1)
19	815.00	(133.9)	521.67	(145.5)	668.34	(138.2)
20	631.25	(103.7)	430.00	(120.0)	530.63	(109.7)
21	676.25	(111.1)	469.17	(130.9)	575.71	(118.4)
L.S.D. - 5% level	133.13		72.74		56.34	
1% level	177.29		96.19		76.56	

Values in brackets are yields in percentage of Chinese whose yield is taken as 100%.

Table 26

AVERAGE YIELDS OF CHINESE AND CHINESE LINES WITH SUBSTITUTED THATCHER, HOPE, AND TIMSTEIN CHROMOSOMES IN 1953 AND 1954

Chromosome tested	THATCHER 1953	THATCHER 1954	HOPE 1953	HOPE 1954	TIMSTEIN 1953	TIMSTEIN 1954	THATCHER	HOPE	TIMSTEIN	LINES
Chinese	547.5	340.0	602.5	380.0	608.8	340.0	443.8	491.2	474.4	469.8
1	1017.5	556.3	875.0	526.3	935.0	545.0	786.9	700.6	740.0	742.5
2	777.5	492.5	627.5	455.0	620.0	482.5	635.0	553.8	551.3	575.8
3	752.5	500.0	645.0	441.3	667.5	445.0	626.3	543.1	556.3	575.2
4	587.5	272.5	662.5	496.3	777.5	486.3	430.0	579.4	631.9	547.1
5	792.5	513.8	735.0	478.8	647.5	468.8	653.1	606.9	558.1	606.0
6	575.0	520.0	747.5	500.0	658.8	467.5	547.5	623.8	563.1	578.1
7	725.0	487.5	807.5	530.0	620.0	480.0	606.3	668.8	550.0	608.3
8	860.0	530.0	770.0	510.0	867.5	527.5	695.0	640.0	697.5	677.5
9	777.5	467.5	750.0	501.3	561.3	421.3	622.5	625.6	491.3	579.8
10	682.5	457.5	727.5	512.5	428.8	427.5	570.0	620.0	553.1	539.4
11	522.5	275.0	552.5	356.3	619.8	413.8	398.8	454.4	516.3	456.5
12	732.5	497.5	877.5	548.8	661.3	452.5	615.0	713.1	556.9	628.3
15	532.5	405.0	625.0	476.3	617.5	370.0	468.8	550.6	493.8	504.4
16	567.5	393.8	567.5	376.3	690.0	493.8	480.6	471.2	591.9	514.8
19	650.0	495.0	625.0	416.3	815.0	427.5	572.5	520.6	671.3	588.1
20	600.0	445.0	602.5	392.5	631.3	420.0	522.5	497.5	525.6	515.2
21	727.5	473.8	777.5	511.3	676.3	425.0	600.6	644.4	550.0	598.5
L.S.D. - 5% level		--	98.9					-- 98.9		- 144.9
1% level		--	130.0					-- 130.0		- 194.6

V. DISCUSSION

The use of substitution lines, as employed in this study, is a new approach to the genetic study of quantitative characters. This method is advantageous where classification of segregants is difficult or impossible and where minor or modifying genes are operating. Hemizygous ineffective recessive genes if present can exert their effect in this material. Although no qualitative characters, such as seed colour, were studied this method is also applicable to such analyses. Since substitution lines can be increased as varieties, tests for as many characters as desired can be carried out. In this study eight characters were tested.

The association of a number of tentative genes on a specific chromosome, as derived from this study, may be considered as a tentative linkage group. These groups have been summarized in Tables 27, 28, and 29. Although linear arrangements within the linkage groups cannot be determined by this method, nevertheless, these genes are linked. This information may be used as a basis for further and more precise linkage studies of these characters. The reason why an indefinite number of genes may be associated with a specific chromosome using substitution lines is that genes are tested against chromosomes and not against linkage testers as used in conventional methods. Thus genes may be found to be linked even though they are more than 50 cross-over units apart.

1. Methods

The establishment of substitution lines entails a considerable amount of cytological work. It is necessary to ascertain the exact chromosomal constitution of both male and female plants at every backcross

generation. Univalent shift in monosomic plants may result in the establishment of a substitution line for a chromosome which has shifted from the bivalent to the univalent condition or it may cause a delay in substitution due to the necessity of discarding the plant material and initiating the program again. This may happen when the members of one or more homologous pairs of chromosomes fail to conjugate or separate precociously. At metaphase, if only one pair of chromosomes is involved, the two homologous univalents may go to one pole and the critical univalent to the other. A gamete of the latter type, if fertilized by a gamete containing the normal complement of chromosomes (21') would result in an individual monosomic for a different chromosome. If monosomics are employed, and they are as males in every backcross generation in producing substitution lines, plants with one univalent only should be used. These plants should be crossed from time to time (best every generation) to standard lines to determine if they are aneuploid for the critical chromosome. Before the program of producing substitution lines is initiated, the donor parent plants to be used in crossing to the nullisomics, monotelosomics, or monoisosomics should be cytologically analyzed to check for presence of chromosomal abnormalities and plants with 21 pairs of chromosomes only should be used.

The number of backcrosses to use in establishing substitution lines may be open to debate. By the fifth backcross generation, approximately 97% of the genes on the 20 chromosomes (excluding the one being transferred) of the non-recurrent parent have been reconstituted. If 3% of the genes at the fifth backcross are in the heterozygous condition there is a possibility that the characters being studied may show heterotic effects, thought slight in self pollinated crops as common wheat,

and erroneous conclusions could be drawn for the character(s) in question. Therefore it may be desirable to backcross for more, probably seven, generations at which time the percentage of genes from the non-recurrent parent will be only approximately 1% and the possibility of heterosis occurring would be almost completely eliminated.

2. Experimental Results

The use of substitution lines simplifies and facilitates considerably the genetic analyses of characters controlled by multiple genes. Each of 19 Thatcher, 16 Hope and 19 Timstein chromosomes were shown to have some effect on at least one character.

Awning was found to be conditioned by genes located on 5 Thatcher, 2 Hope and 3 Timstein chromosomes. The results for chromosomes VIII, IX, and X substantiate previous findings (Sears 71, Unrau 102, O'Mara 58). The association of genes with chromosomes III of Thatcher and Timstein and IV, XII, and XXI of Thatcher was not expected on the basis of previous information. To account for the appearance of awning in substitution lines III, IV, XII, and XXI, an extension of the present theory is proposed (see IV. 1, above). To determine whether a single gene may be responsible for a chromosome's action and whether the gene action is dominant or recessive, crosses may be made between each of the substitution lines III, IV, XII, and XXI and the recipient variety. Only genes on one chromosome pair will segregate. If F_1 plants are awnless then Chinese carries the dominant alleles and if F_1 plants are awned then awn promoting genes are dominant and Chinese possesses recessive alleles. F_2 segregation would show whether one or more genes were operating in conditioning awning. Similar types of crosses between any substitution line and the recipient parent may be made for any character to determine whether one or more genes are responsible for a chromosome's action.

Studies of earliness (IV. 2., above) indicate that time of heading is conditioned by two types of genes: (a) those that differentiate summer and winter growth habits and (b) those that modify the expression of growth habit genes to a greater or lesser extent. Unrau (102) associated

one recessive gene for winter growth in Hymar with chromosome IX. Two other genes for winter growth habit have been associated in this study, with chromosomes XIII and XVIII of Thatcher. Therefore alleles at at least 3 loci condition winter growth habit. The modifying genes appear to be multiple and of varying strengths. Ten chromosomes each of Thatcher and Hope, and 13 of Timstein have significant enhancing effects.

Genes on 3 Thatcher, 6 Hope, and 1 Timstein chromosome appear to have a marked effect on plant height (IV. 3., above). Increase in plant height is due to a gene or genes on chromosome XI of Thatcher, Chromosomes I, III, VII, IX, and XII of Hope, VIII of Thatcher, Hope, and Timstein, and XVI of Thatcher seem to possess genes reducing plant height of Chinese. These results substantiate (indirectly) previous findings of Goulden (30), Thompson (99), and Sears (71).

From results of other investigators and those of this study, (IV. 6., above) it seems that two types of genes, which may be classified as major and minor or modifying genes, condition spike density in 21" chromosome wheats. Major genes differentiate between dense and lax spikes as in interspecific crosses between <u>compactum</u> and <u>vulgare</u> wheats. In intraspecific crosses the degree of density depends on minor or modifying genes. Since substitution lines were produced using only intraspecific varieties, only minor gene differences would be expected on the basis of this assumption. The results obtained substantiate the assumption. Chromosomes IV of Thatcher, II of Hope, and XII of Timstein increased significantly spike density of Chinese; eight Thatcher, three Hope, and eleven Timstein chromosomes reduced Chinese spike density. The minor or modifying genes on different chromosomes within varieties gave in certain comparisons significantly different genetic effects. That substitution lines may be used in analyzing characters for minor

or modifying genes seems to be supported by results for this character.

Studies of lodging, protein content, thousand-kernel weight and yield (IV. 5, 4, 7, 8, above) reveal that numerous chromosomes condition the expression of these characters. In contrast to characters such as awning, earliness, and spike density which are conditioned by both major genes with large effects and minor genes with small effects, these characters, together with plant height, seem to be controlled by the joint action of a large number of genes, each with a small effect. Although the individual effects of these polygenes are similar they are not necessarily equal. Protein content in Thatcher was found to be conditioned by 5 chromosomes. The genetic effects of these chromosomes were apparently equal. Lodging was conditioned by 15 Thatcher, 13 Hope, and 9 Timstein chromosomes; the effects of chromosomes within varieties were not always equal. The same was true for chromosomal effects for thousand-kernel weight and yield. Kernel weight was conditioned by 3 Thatcher, 3 Hope and 5 Timstein chromosomes. The number of chromosomes affecting yield was large, 4 in Thatcher, 10 in Hope, and 14 in Timstein. The genetic effects of individual chromosomes were more variable for this character than for any other.

Since whole chromosomes are being tested, it is impossible, before further work is carried out, to predict whether the chromosome effect on any character is due to one or more genes. Where substitution lines are not significantly different from Chinese this similarity may be due to absence of pertinent genes on chromosomes concerned or similarity of alleles in both the recipient and donor varieties. Where differences are significant this may be due to one or more differential genes per chromosome. If one gene conditions a character it may have one, two, or a series of alleles. If two or more genes per chromosome

condition a character they also may have one, two or a series of alleles each and the situation becomes increasingly difficult to analyze. If multiple alleles exist and two or more genes affecting a particular character are carried by any one chromosome, testing may reveal no more than the expression of the particular genic combination of the transferred chromosome.

For earliness, height, lodging, spike density, and yield, it was possible to calculate a lines x varieties interaction which in all cases was highly significant. These significant values show that genetic effects of some of the homologous chromosomes of different varieties are significantly different genetically and may support either of two alternatives: (a) the action of a chromosome is due to one gene with two or a series of alleles for each, the alleles being carried by homologous chromosomes of different varieties; or (b) the action of a chromosome is due to more than one gene and the transferred chromosome has a combination of genes different from that of its Chinese homologue.

Since numerous genes condition certain characters, their multiplicity may have originated in the following ways. Duplication or even triplication is thought to be the main cause for a high degree of multiplicity. Gene and chromosomal mutations also may be responsible for adding genes to a polygenic system. Mutations of duplicate or even triplicate genes are probably the cause of multiple allelic series.

On the basis of results, there is considerable promise that the chromosome substitution method will permit a more adequate understanding of the genetics of quantitative characters. It appears that by transferring whole chromosomes it should be possible to improve existing varieties with genes for desirable characters from other varieties without going through testing procedures until the transfer is completed. Such

a method would permit the breeding of such characters as rust resistance without rust nurseries. Whether whole chromosome substitution will become a useful method of plant breeding depends on: (a) the autonomous or non-autonomous action of genes in different genic milieu, and (b) sufficiency of fairly easily transferrable characters. The larger the number of genes involved in conditioning a particular character, the more difficult it would be to transfer the character and thus the less useful the method as a plant breeding tool.

VI SUMMARY

Thatcher, Hope, and Timstein substitution lines were tested to determine the association between the various chromosomes and the characters, awning, earliness, height, lodging, protein content, spike density, thousand-kernel weight, and yield.

1. Awning was apparently conditioned by 2 genes in Hope, 3 in Timstein, and 5 in Thatcher. In Hope, the recessive alleles hd and b_2 of the two awn-inhibiting genes of Chinese were associated with chromosomes VIII and X; chromosome IX also possesses b_1 as does Chinese. Timstein also appears to carry the alleles hd and b_2 on chromosome VIII and X; chromosome IX carries the dominant awn-inhibiting gene B_1 or a slightly less effective allele $B_1{}^a$. An awn promoting gene (K or k) was associated with chromosome III of Timstein. Thatcher carries hd or Hd^a on VIII, $b_1{}^a$ on IX and b_2 on X. The appearance of awned types in lines III, IV, XII, and XXI was not expected to the basis of published information; a hypothesis is proposed to explain the results. Chromosomes III, IV, and XXI may carry either dominant or recessive awn-promoting alleles.

2. Earliness was conditioned by 2 types of genes: (a) those differentiating summer and winter growth habit, and (b) those modifying the expression of each gene type in (a). Chinese, Hope, and Timstein each carry summer growth habit genes on chromosomes XIII and XVIII; Thatcher carries winter growth habit genes on these chromosomes possibly at the same loci. Genes on Thatcher chromosomes I, II, III, V, VI, VIII, IX, XII, XXI, Hope chromosomes II, III, IV, V, VII, IX, X, XII, XVIII, XXI, and Timstein chromosomes II, III, IV, VI, V, VII, VIII, IX, XII, XVII, XVIII, XIX, and XX modified more or less the earliness of Chinese. The modifications were all in the direction of enchanced earliness.

3. Eight genes or groups of genes seem to condition plant height. Chromosome XI of Thatcher was associated with significant height increase. Chromosomes I, III, VII, IX, and XII of Hope, VIII of Thatcher, Hope and Timstein and XVI of Thatcher were associated with significant height decrease of Chinese.

4. Thatcher chromosomes I, II, III, IV, V, VI, VII, VIII, IX, XII, XIII, XVI, XIX, XX, XXI, Hope chromosomes I, II, III, IV, V, VI, VII, VIII, IX, XII, XVII, XIX, XX, and Timstein chromosomes I, IV, VIII, V, IX, X, XV, XVIII, and XIX each produced lines significantly more resistant to lodging than Chinese. The different chromosomes within any set of substitution lines do not effect lodging equally. Chromosomes with major and minor genetic effects appear to be present. None of the substitution lines of either of the three sets were significantly lower than Chinese in lodging resistance.

5. Protein content of Thatcher was found to be conditioned by genes associated with chromosomes V, VII, IX, XV, and XVI. These chromosomes were associated with a significant increase in protein content in their respective Chinese lines.

6. Differences in spike density between the donor varieties Thatcher, Hope, and Timstein and the recipient variety of Chinese were due to minor or modifying genes; no major gene differences were obtained. These modifying genes which were associated with Thatcher chromosomes I, III, IV, VI, VIII, IX, X, XIX, XXI, Hope chromosomes II, VIII, X, XX, and Timstein chromosomes III, V, VI, VII, VIII, X, XI, XII, XVI, XIX, XX, and XXI showed varying degress of effects.

7. At least 7 chromosomes, I, V, XVI, of Thatcher, I, IV, VI, of Hope, and I, V, VI, X, XIX, of Timstein condition kernel weight. Chromosome lines I, IV, V, VI, X, and XIX, were associated with a significant increase in kernel weight over Chinese. Chinese XVI Thatcher lines were significantly lower than Chinese. Chromosome I had the greatest effect, involving all three donor varieties; in every case kernel size was significantly increased.

8. Yield was conditioned by Thatcher chromosomes I, III, VIII, XII, Hope chromosomes IV, V, VI, VII, VIII, IX, X, XII, XXI, and Timstein chromosomes I, II, III, IV, V, VI, VII, VIII, XII, XVI, XVII, XVIII, XIX and XXI. Chromosome lines within each of the three sets of substitution lines showed both major and minor genetic effects. Significantly higher yielding lines gave yield increases over Chinese ranging from 12.0 to 58.6 per cent.

9. The advantages and limitations of substitution lines for cytogenetic studies and plant breeding are discussed.

TABLE 27

ASSOCIATION OF INDIVIDUAL THATCHER CHROMOSOMES WITH THE CHARACTERS STUDIED

Chromosome tested		Awning	Earliness	Height	Lodging	Protein Content	Spike Density	1,000-Kernel Weight	Yield
1.	*S.H.		+		+			+	+
	**S.L.						+		
2.	S.H.		+		+				
	S.L.								
3.	S.H.	+	+		+				+
	S.L.						+		
4.	S.H.	+			+		+		
	S.L.								
5.	S.H.		+		+	+		+	
	S.L.								
6.	S.H.		+		+				
	S.L.						+		
7.	S.H.		+		+	+			
	S.L.								
8.	S.H.	+	+		+				+
	S.L.			+			+		
9.	S.H.	+	+		+	+			
	S.L.						+		
10.	S.H.	+							
	S.L.						+		
11.	S.H.			+					
	S.L.								
12.	S.H.	+	+		+				+
	S.L.								
13.	S.H.				+				
	S.L.		+						
15.	S.H.		+			+			
	S.L.								
16.	S.H.				+	+			
	S.L.			+				+	
18.	S.H.								
	S.L.		+						
19.	S.H.				+				
	S.L.						+		
20.	S.H.				+				
	S.L.								
21.	S.H.	+			+				
	S.L.						+		

* Significantly Higher - S.H.
** Significantly Lower - S.L.

[illegible]

[illegible]

[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

[illegible]

[illegible]

TABLE 28

ASSOCIATION OF INDIVIDUAL HOPE CHROMOSOMES WITH THE CHARACTERS STUDIED

Chromosome tested		Awning	Earliness	Height	Lodging	Spike Density	1,000-Kernel Weight	Yield
1.	*S.H.				+		+	+
	**S.L.			+				
2.	S.H.		+		+	+		
	S.L.							
3.	S.H.		+		+			
	S.L.			+				
4.	S.H.		+		+		+	+
	S.L.							
5.	S.H.		+		+			+
	S.L.							
6.	S.H.				+		+	+
	S.L.							
7.	S.H.		+		+			+
	S.L.			+				
8.	S.H.	+			+	+		+
	S.L.			+				
9.	S.H.		+		+			+
	S.L.			+				
10.	S.H.	+	+					+
	S.L.					+		
11.	S.H.							
	S.L.							
12.	S.H.		+		+			+
	S.L.			+				
15.	S.H.							
	S.L.							
16.	S.H.							
	S.L.							
17.	S.H.				+			
	S.L.							
18.	S.H.		+					
	S.L.							
19.	S.H.				*			
	S.L.							
20.	S.H.				+			
	S.L.					+		
21.	S.H.		+					+
	S.L.							

* Significantly Higher - S.H.
** Significantly Lower - S.L.

[illegible]

[illegible]

[illegible]

[illegible]

TABLE 29

ASSOCIATION OF INDIVIDUAL TIMSTEIN CHROMOSOMES WITH THE CHARACTERS STUDIED

Chromosome tested		Awning	Earliness	Height	Lodging	Spike Density	1,000-Kernel Weight	Yield
1.	*S.H.				+		+	+
	**S.L.							
2.	S.H.		+					+
	S.L.							
3.	S.H.	+	+			+		+
	S.L.							
4.	S.H.		+		+			+
	S.L.							
5.	S.H.		+		+	+	+	+
	S.L.							
6.	S.H.		+			+	+	+
	S.L.							
7.	S.H.		+			+		+
	S.L.							
8.	S.H.	+	+		+	+		+
	S.L.			+				
9.	S.H.		+		+			
	S.L.							
10.	S.H.	+			+	+	+	
	S.L.							
11.	S.H.					+		
	S.L.							
12.	S.H.		+			+		+
	S.L.							
15.	S.H.				+			
	S.L.							
16.	S.H.					+		+
	S.L.							
17.	S.H.		+					+
	S.L.							
18.	S.H.		+		+			+
	S.L.							
19.	S.H.		+		+	+	+	+
	S.L.							
20.	S.H.		+			+		
	S.L.							
21.	S.H.					+		+
	S.L.							

* Significantly Higher - S.H.
** Significantly Lower - S.L.

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IX. APPENDIX

Table 1

Computation of lines x years interaction of earliness from composite of 3 sets of substitution lines in 1953 and 1954.

	Thatcher						Hope						Timstein					
	*1954[1]		*1954[2]		1953		1954[1]		1954[2]		1953		1954[1]		1954[2]		1953	
Chromosome tested	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2
Chinese Spring	65	65	69	67	66	66	65	65	67	67	67	67	65	65	67	68	66	66
1	58	67	62	62	63	63	64	63	66	66	67	66	64	66	67	68	66	66
2	58	59	64	63	64	64	55	55	62	62	64	64	62	60	65	64	68	67
3	57	57	62	62	63	63	53	54	61	62	62	62	62	63	66	67	65	64
4	64	63	68	69	66	67	58	59	64	62	66	65	64	63	66	67	65	66
5	59	59	63	63	64	64	57	59	62	63	64	65	61	61	63	63	63	64
6	57	57	63	62	63	63	60	62	65	65	63	65	61	61	62	62	63	64
7	59	58	64	64	63	64	50	50	59	60	60	60	63	62	67	67	65	65
8	58	58	63	63	63	63	63	64	66	66	65	65	61	61	61	62	64	64
9	61	61	67	68	63	63	53	53	62	62	62	62	63	62	64	65	69	67
10	62	63	68	68	66	66	53	53	62	61	62	62	62	62	65	67	70	70
11	65	65	68	68	66	67	62	63	67	67	68	67	62	63	67	67	66	66
12	57	57	62	62	63	63	56	55	63	63	63	64	60	60	62	62	63	63
15	64	63	66	67	66	66	61	62	67	67	66	66	64	65	67	68	67	67
16	64	64	66	66	66	66	63	63	68	67	66	67	66	66	68	67	66	66
19	62	63	67	67	66	67	64	65	67	67	73	73	64	63	67	65	65	66
20	61	60	66	66	64	64	64	65	66	67	65	65	63	62	65	64	64	63
21	63	62	66	66	66	66	56	55	61	62	64	64	65	66	67	67	67	67

Table 1 (continued)

Analysis of Variance

Source of Variation	df	ss	ms	F	5%	1%
Total	323	3834.8				
Reps	1	1.6	1.6			
Varieties	2	210.4	105.2			
Years	2	1193.0	596.5			
YxV	4	117.6	29.4			
Error (1)	8	2.7	0.3			
Lines	17	998.8	58.8			
LxY	34	204.5	6.0	0.25	1.77	2.25
LxV	34	808.1	23.8	7.68^{xx}	1.60	1.94
LxYxV	68	208.9	3.1	6.89^{xx}	1.38	1.58
Error (2)	153	69.2	0.45			

	LxYxV	LxV	L
L.S.D. 5% level	1.325	1.996	3.314
1% level	1.752	2.651	4.450

*1954[1] test at Edmonton
*1954[2] test at Brooks

Table 2

Computation of lines x varieties interaction of earliness from composite of 3 sets of substitution lines in 1953.

Chromosome tested	Hope				Ave.	Timstein				Ave.	Thatcher (1)				Ave.
Chinese Spring	67	67	67	66	66.75	66	66	67	66	66.25	66	66	66	65	66.25
1	67	66	67	66	66.50	66	66	65	66	65.75	63	63	63	63	63.00
2	64	64	65	64	64.25	68	67	64	67	66.50	64	64	64	64	64.00
3	62	62	63	62	62.25	65	64	65	64	64.50	63	63	63	63	63.00
4	66	65	64	64	64.75	65	66	66	65	65.50	66	67	66	66	66.25
5	64	65	65	64	64.50	63	64	64	67	64.50	64	64	64	64	64.00
6	63	65	65	65	64.50	63	64	63	63	63.25	63	63	63	63	63.00
7	60	60	60	60	60.00	65	65	65	66	65.25	63	64	64	64	63.75
8	65	65	66	65	65.25	64	64	64	64	64.00	63	63	64	64	63.50
9	62	62	62	63	62.25	69	67	68	69	68.25	63	63	63	63	63.00
10	62	62	62	63	62.25	70	70	70	70	70.00	66	66	66	66	66.00
11	68	67	66	66	66.75	66	66	66	66	66.00	66	67	67	67	66.75
12	63	64	64	64	63.75	63	63	62	63	62.75	63	63	63	63	63.00
15	66	66	65	65	65.50	67	67	67	68	67.25	66	66	65	65	65.50
16	66	67	67	66	66.50	66	66	66	67	66.25	66	66	66	67	66.25
19	73	73	73	73	73.00	65	66	65	66	65.50	66	67	67	67	66.75
20	65	65	65	65	65.00	64	63	63	64	63.50	64	64	64	64	64.00
21	64	64	63	64	63.75	67	67	66	68	67.00	66	66	66	66	66.00

Analysis of Variance

Source	df	ss	ms	F	0.05	0.01
Total	215	9154000.0				
Reps	3	1.4	0.47			
Varieties	2	40.4	20.20			
Error (1)	6	4.7	0.78			
Lines	17	419.6	24.68			
Lines x varieties	34	462.1	13.59	41.18xx	1.51	1.79
Error (2)	153	50.9	0.33			

L.S.D. 5% level - 0.80
1% level - 1.06

Table 3

Computation of lines x varieties interaction of earliness from composite of 3 sets of substitution lines in 1954 at Edmonton.

Chromosome tested	Hope		Ave.	Timstein		Ave.	Thatcher		Ave.
Chinese Spring	65	65	65.0	65	65	65.0	65	65	65.0
1	64	63	63.5	64	66	65.0	58	57	57.5
2	55	55	55.0	62	60	61.0	58	59	58.5
3	53	54	53.5	62	63	62.5	57	57	57.0
4	58	59	58.5	64	63	63.5	64	63	63.5
5	57	59	58.0	61	61	61.0	59	59	59.0
6	60	62	61.0	61	61	61.0	57	57	57.0
7	50	50	50.0	63	62	62.5	59	58	58.5
8	63	64	63.5	61	61	61.0	58	58	58.0
9	53	53	53.0	63	62	62.5	61	61	61.0
10	53	53	53.0	62	62	62.0	62	63	62.5
11	62	63	62.5	62	63	62.5	65	65	65.0
12	56	55	55.5	60	60	60.0	57	57	57.0
15	61	62	61.5	64	65	64.5	64	63	63.5
16	63	63	63.0	66	66	66.0	64	64	64.0
18	58	59	58.5	61	62	61.5	90	90	90.0
19	64	65	64.5	64	63	63.5	62	63	62.5
20	64	65	64.5	63	62	62.5	61	60	60.5
21	56	55	55.5	65	66	65.5	63	62	62.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	113	428597.4				
Reps	1	0.3	0.30			
Varieties	2	332.6	166.30		1.64	2.00
Error (1)	2	2.1	1.05			
Lines	18	1119.6	62.20			
Lines x varieties	36	1707.4	47.43	124.82xx		
Error (2)	54	20.6	0.38			

L.S.D. 5% level - 1.24

1% level - 1.65

Table 3A

Computation of lines x varieties interaction of earliness from composite of 3 sets of substitution lines in 1954 at Brooks.

Chromosome tested	Hope						Ave.	Timstein						Ave.	Thatcher						Ave.
Chinese Spring	67	67	67	67	67	67	67.0	67	68	67	67	67	68	67.3	69	67	67	68	67	67	67.5
1	66	66	66	66	67	66	66.1	67	68	67	67	67	67	67.1	62	62	62	62	62	61	61.8
2	62	62	62	62	62	62	62.0	65	64	64	64	65	65	64.5	64	63	62	62	62	62	62.5
3	61	62	62	62	62	62	61.8	66	67	67	66	67	67	66.6	62	62	62	62	62	62	62.0
4	64	62	62	62	63	62	62.5	66	67	66	67	67	66	66.5	68	69	68	68	68	68	68.1
5	62	63	62	62	63	62	62.3	63	63	63	63	63	63	63.0	63	63	63	62	63	63	62.8
6	65	65	65	65	65	65	65.0	62	62	63	63	65	64	63.1	63	62	63	63	62	62	62.5
7	59	60	60	60	60	60	59.8	67	67	65	66	66	66	66.1	64	64	63	63	63	63	63.3
8	66	66	66	65	64	66	66.0	61	62	63	62	63	62	62.1	63	63	62	61	62	61	62.0
9	62	62	62	62	62	62	62.0	64	65	67	65	65	65	65.1	67	68	67	67	66	66	66.8
10	62	61	62	62	62	62	61.8	65	67	65	65	66	67	65.8	68	68	67	67	67	67	67.3
11	67	67	68	67	67	67	67.1	67	67	67	68	67	68	67.3	68	68	68	68	67	67	67.7
12	63	63	61	62	62	62	62.1	62	62	62	62	62	62	62.0	62	62	62	61	62	61	61.7
15	67	67	66	67	67	67	66.8	67	68	67	67	67	67	67.1	66	67	66	66	66	65	66.0
16	68	67	67	67	67	67	67.1	68	67	67	67	67	67	67.1	66	66	67	67	67	66	66.5
18	62	61	61	62	62	62	61.7	63	62	62	62	64	63	62.6	88	88	88	88	88	88	88.0
19	67	67	67	67	67	67	67.0	67	65	66	65	67	66	66.0	67	67	66	66	67	66	66.5
20	66	67	67	67	66	67	66.7	65	64	64	64	65	65	64.5	66	66	65	65	65	66	65.5
21	61	62	61	62	62	62	61.7	67	67	67	67	67	68	67.1	66	66	65	65	65	65	65.3

Analysis of Variance

Source	df	ss	ms	F	0.05	0.01
Total	341					
Reps	5	3.8	0.76			
Varieties	2	233.0	116.5			
Error (1)	10	11.2	1.12			
Lines	18	1501.4	83.4			
Lines x varieties	36	3227.1	89.6	30.90xx	1.47	1.71
Error (2)	270	78.4	0.29			

L.S.D. 5% level - 0.62
1% level - 0.82

TABLE 4

Chinese Spring lines with substituted Thatcher chromosomes.

1952

Chromosome tested	Earliness Series 1	Series 2	Series 3	Series 4	Average
Chinese Spring	69	69	69	69	69.0
Thatcher	63	63	63	63	63.0
1	64	65	64	64	64.25
2	66	66	66	66	66.0
3	64	64	64	64	64.0
4	68	68	68	68	68.0
5	66	66	66	66	66.0
6	64	65	65	65	64.75
7	66	66	66	66	66.0
8	65	65	66	65	65.25
9	64	64	64	64	64.0
10	66	66	66	66	66.0
11	69	69	69	68	68.75
12	64	64	64	65	64.25
15	66	66	66	66	66.0
16	72	72	72	72	72.0
17	68	68	68	68	68.0
19	68	68	68	68	68.0
20	66	66	66	67	66.25
21	68	69	68	69	68.50

Analysis of Variance

Source	D.F.	S.S.	M.S.	F	5%	1%
Total	79	377				
Reps	3	0	0			
Lines	19	372	19.6	217.7xx	1.77	2.25
Error	57	5	0.09			

L.S.D. (1) 5% - $t.05 \times \sqrt{\frac{2\times .09}{4}} = 0.424424$

(11) 1% - $t.01 \times \sqrt{\frac{2\times .09}{4}} = .212 \times 2.666 = 0.565192$

TABLE 5

Chinese Spring lines with substituted Thatcher chromosomes.

Chromosome tested	Earliness Series 1	Series 2	Series 3	Series 4	Average	1953
Thatcher	61	61	61	61	61.00	
Chinese Spring	66	66	66	67	66.25	
1	63	63	63	63	63.00	
2	64	64	64	64	64.00	
3	63	63	63	63	63.00	
4	66	67	66	66	66.25	
5	64	64	64	64	64.00	
6	63	63	63	63	63.00	
7	63	64	64	64	63.75	
8	63	63	64	64	63.50	
9	63	63	63	63	63.00	
10	66	66	66	66	66.00	
11	66	67	67	67	66.75	
12	63	63	63	63	63.00	
13	77	78	77	79	77.75	
15	66	66	65	65	65.50	
16	66	66	66	67	66.25	
17	66	66	67	66	66.25	
18	83	83	83	83	83.00	
19	66	67	67	67	66.75	
20	64	64	64	64	64.00	
21	66	66	66	66	66.00	

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	87	2098				
Reps	3	1.2	0.40	2.86		
Lines	21	2088	99.43	710^{xx}	1.73	2.17
Error	63	8.8	0.14			

L.S.D. - 5% point = .26 x 2.001 = 0.520
1% point = .26 x 2.663 = 0.692

TABLE 6

Chinese Spring lines with substituted Thatcher chromosomes.

Earliness 1954

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Series 5	Series 6	Average	Total
Thatcher	59	59	58	58	59	59	58.7	352
Chin. Spring	69	67	67	68	67	67	67.5	405
1	62	62	62	62	62	61	61.8	371
2	64	63	62	62	62	62	62.5	375
3	62	62	62	62	62	62	62.0	372
4	68	69	68	68	68	68	68.1	409
5	63	63	63	62	63	63	62.8	377
6	63	62	63	63	62	62	62.5	375
7	64	64	63	63	63	63	63.3	380
8	63	63	62	61	62	61	62.0	372
9	67	68	67	67	66	66	66.8	401
10	68	68	67	67	67	67	67.3	404
11	68	68	68	68	67	67	67.7	406
12	62	62	62	61	62	61	61.7	370
13	88	88	88	88	88	88	88.0	528
15	66	67	66	66	66	65	66.0	396
16	66	66	67	67	67	66	66.5	399
18	88	88	88	88	88	88	88.0	528
19	67	67	66	66	67	66	66.5	399
20	66	66	65	65	65	66	65.5	393
21	66	66	65	65	65	65	65.3	392
22(10)	67	68	67	67	66	67	67.0	402
23(16)	65	65	65	65	66	66	65.3	392
24(19)	67	67	67	67	67	68	67.1	403
Tim.	57	56	57	57	56	56	56.5	339

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	7455.4				
Reps	5	7.9	1.58			
Lines	24	7417.4	309.1	1236.4	1.61	1.95
Error	120	30.1	.25			

L.S.D. - 5% point-1.982 x .29 = 0.475

- 1% point-2.621 x .29 = 0.760

TABLE 7

Chinese Spring lines with substituted Thatcher chromosomes.

1954

Chromosome tested	Earliness Series 1	Series 2	Total	Average
Thatcher	54	54	108	54.0
Chinese Spring	65	65	130	65.0
1	58	57	115	57.5
2	58	59	117	58.5
3	57	57	114	57.0
4	64	63	127	63.5
5	59	59	118	59.0
6	57	57	114	57.0
7	59	58	117	58.5
8	58	58	116	58.0
9	61	61	122	61.0
10	62	63	125	62.5
11	65	65	130	65.0
12	57	57	114	57.0
13	90	90	180	90.0
15	64	63	127	63.5
16	64	64	128	64.0
18	90	90	180	90.0
19	62	63	125	62.5
20	61	60	121	60.5
21	63	62	125	62.5
22(10)	62	63	125	62.5
23(16)	63	64	127	63.5
24(19)	63	63	126	63.0

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	47	3654				
Reps	1	0				
Lines	23	3548.5	154.2	230.2**	2.01	2.72
Error	23	15.5	.67			

L.S.D. 5% point – $2.00 \times \sqrt{2 \times .67} = .66 \times 2.07 = 1.36$

1% point – $2.66 \times \sqrt{2 \times .67} = .66 \times 2.81 = 1.85$

TABLE 8

Chinese Spring lines with substituted Hope chromosomes.

Earliness

1953

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Average
*Hope	67	67	67	67	67.00
Chinese Spring	67	67	67	66	66.75
1	67	66	67	66	66.50
2	64	64	65	64	64.25
3	62	62	63	62	62.25
4	66	65	64	64	64.25
5	64	65	65	64	64.50
6	63	65	65	65	64.50
7	60	60	60	60	60.00
8	65	65	66	65	65.25
9	62	62	62	63	62.25
10	62	62	62	63	62.25
11	68	67	66	66	66.75
12	63	64	64	64	63.75
15	66	66	65	65	65.50
16	66	67	67	66	66.50
17	67	66	66	66	66.25
*19	73	73	73	73	73.00
20	65	65	65	65	65.00
21	64	64	63	64	63.75

* germinated approximately 8 days later than other lines

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	549				
Reps	3	1	0.333	1.05		
Lines	19	530	27.8	88.0xxx	1.77	2.25
Error	57	18	0.316			

L.S.D. (1) 5% - $t_{.05} \times \sqrt{\frac{2 \times .316}{4}} = 2.002 \times 0.396 = .792792$

(11) 1%- $t_{.01} \times \sqrt{\frac{2 \times .316}{4}} = 2.666 \times 0.396 = 1.055736$

TABLE 9

Chinese Spring lines with substituted Hope chromosomes

Earliness 1954

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Total	Average
Hope	55	55	55	55	220	55.00
Chinese Spring	65	65	66	65	261	65.25
1	64	63	64	64	255	63.75
2	55	55	56	54	220	55.00
3	53	54	54	54	215	53.75
4	58	59	60	59	236	59.00
5	57	59	59	58	233	58.25
6	60	62	61	61	244	61.00
7	50	50	50	50	200	50.00
8	63	64	64	64	255	63.75
9	53	53	53	53	212	53.00
10	53	53	54	54	214	53.50
11	62	63	63	64	252	63.00
12	56	55	56	55	222	55.50
15	61	62	62	62	247	61.75
16	63	63	63	62	251	62.75
17	61	62	63	61	247	61.75
18	58	59	59	58	234	58.50
19	64	65	65	65	259	64.75
20	64	65	65	66	260	65.00
21	56	55	55	55	221	55.25

Analysis of Variance

Source	df	ss	ms	F	0.05-	0.01
Total	83	1770				
Reps	3	6.3	2.1			
Lines	20	1745	87.25	281.4xx	1.75	2.20
Error	60	18.7	.31			

L.S.D. (1) 5% point - $t_{.05} \times \sqrt{\frac{2 \times .31}{4}} = 2.00 \times .39 = 0.78$

(11) 1% point - $t_{.01} \times \sqrt{\frac{2 \times .31}{4}} = 2.66 \times .39 = 1.04$

TABLE 10

Chinese Spring lines with substituted Hope chromosomes

Earliness 1954

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Series 5	Series 6	Average	Total
Hope	62	62	62	62	62	62	62.0	372
Chin. Spring	67	67	67	67	67	67	67.0	402
1	66	66	66	66	67	66	66.1	397
2	62	62	62	62	62	62	62.0	372
3	61	62	62	62	62	62	61.8	371
4	64	62	62	62	63	62	62.5	375
5	62	63	62	62	63	62	62.5	374
6	65	65	65	65	65	65	65.0	390
7	59	60	60	60	60	60	59.8	359
8	66	66	66	65	67	66	66.0	396
9	62	62	62	62	62	62	62.0	372
10	62	61	62	62	62	62	61.8	371
11	67	67	68	67	67	67	67.1	403
12	63	63	61	62	62	62	62.1	373
15	67	67	66	67	67	67	66.8	401
16	68	67	67	67	67	67	67.1	403
17	67	66	66	66	66	66	66.1	397
18	62	61	61	62	62	62	61.7	370
19	67	67	67	67	67	67	67.0	402
20	66	67	67	67	66	67	66.7	400
21	61	62	61	62	62	62	61.7	370
Thatcher	59	58	58	58	58	58	58.1	349
Timstein	57	56	57	57	56	56	56.5	339
Regent	56	57	57	56	57	56	56.5	339
Red Bobs	59	58	58	58	58	58	58.1	349

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	1704				
Reps	5	1	.20	349.75^{xx}		
Lines	24	1679	69.96		1.61	1.95
Error	120	24	.20			

L.S.D. 5 % point $1.982 \times \sqrt{\frac{2 \times .20}{6}} \times (.258) = .511$

1% point $2.621 \times \sqrt{\frac{2 \times .20}{6}} \times .258 = .676$

TABLE 11

Chinese Spring lines with substituted Timstein chromosomes.

Earliness

1953

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Average
Timstein	60	60	60	60	60.00
Chinese Spring	66	66	67	66	66.25
1	66	66	65	66	65.75
2	68	67	64	67	66.50
3	65	64	65	64	64.50
4	65	66	66	65	65.50
5	63	64	64	67	64.50
6	63	64	63	63	63.25
7	65	65	65	66	65.25
8	64	64	64	64	64.00
9	69	67	68	69	68.25
*10	70	70	70	70	70.00
11	66	66	66	66	66.00
12	63	63	62	63	62.75
15	67	67	67	68	67.25
16	66	66	66	67	66.25
17	65	65	65	65	65.00
18	65	66	65	65	65.25
19	65	66	65	66	65.50
20	64	63	63	64	63.50
21	67	67	66	68	67.00

* poor germination which was approximately 5 days later than other lines

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	379				
Reps	3	4	1.33	2.75		
Lines	20	346	17.3	35.8^{xx}	1.75	2.20
Error	60	29	0.483			

L.S.D. (1) 5% point $= t.05 \times \sqrt{\frac{2x\ .483}{4}} = 2.00 \times 0.491 = 0.982$

(11)1% point $- t.01 \times \sqrt{\frac{2 \times .483}{4}} = 2.66 \times 0.491 = 1.30606$

TABLE 12

Chinese Spring lines with substituted Timstein chromosomes.

Earliness 1954

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Total	Average
Timstein	51	51	51	51	204	51.00
Chinese Spring	65	65	65	66	261	65.25
1	64	66	65	65	260	65.00
2	62	60	59	59	240	60.00
3	62	63	62	61	248	62.00
4	64	63	64	63	254	63.50
5	61	61	61	60	243	60.75
6	61	61	61	62	245	61.25
7	63	62	63	63	251	62.75
8	61	61	61	58	241	60.25
9	63	62	61	62	248	62.00
10	62	62	63	62	249	62.25
11	62	63	63	64	252	63.00
12	60	60	59	59	238	59.50
15	64	65	65	65	259	64.75
16	66	66	66	66	264	66.00
17	64	63	63	62	252	63.00
18	61	62	62	60	245	61.25
19	64	63	63	63	253	63.25
20	63	62	62	62	249	62.25
21	65	66	66	66	263	65.75

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	835.6				
Reps	3	2.4				
Lines	20	801.3	40.1	75.6^{xx}	1.75	2.20
Error	60	31.9	0.53			

L.S.D. $t_{.05} \times \sqrt{\frac{2 \times .053}{4}} = 2.00 \times .51 = 1.02$

$t_{.01} \times \sqrt{\frac{2 \times .053}{4}} = 2.66 \times 51 = 1.36$

TABLE 13

Chinese Spring lines with substituted Timstein chromosomes.

Earliness 1954

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Series 5	Series 6	Average	Total
Timstein	57	57	57	56	57	57	56.8	341
Chin. Spring	67	68	67	67	67	68	67.3	404
1	67	68	67	67	67	67	67.1	403
2	65	64	64	64	65	65	64.5	387
3	66	67	67	66	67	67	66.6	400
4	66	67	66	67	67	66	66.5	399
5	63	63	63	63	63	63	63.0	378
6	62	62	63	63	65	64	63.1	379
7	67	67	65	66	66	66	66.1	397
8	61	62	63	62	63	62	62.1	373
9	64	65	67	65	65	65	65.1	391
10	65	67	65	65	66	67	65.8	395
11	67	67	67	68	67	68	67.3	404
12	62	62	62	62	62	62	62.0	372
15	67	68	67	67	67	67	67.1	403
16	68	67	67	67	67	67	67.1	403
17	66	66	66	65	66	65	65.6	394
18	63	62	62	62	64	63	62.6	376
19	67	65	66	65	67	66	66.0	396
20	65	64	64	64	65	65	64.5	387
21	67	67	67	67	67	68	67.1	403
Thatcher	58	58	58	58	58	58	58.0	348
Red Bobs	59	58	58	58	58	58	58.1	349
Regent	57	57	56	57	57	57	56.8	341
Reward	58	58	58	58	58	58	58.0	348

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	1911.5				
Reps	5	4	0.80			
Lines	24	1866.3	77.76	226.7	1.61	1.95
Error	120	41.2	.343			

L.S.D. 5% point - 1.982 x .388 = 1.16

1% point - 2.621 x .586 = 1.54

Table 14

Computation of lines x years interaction of plant height from composite of 3 sets of substitution lines in 1953 and 1954.

	Hope				Timstein				Thatcher			
	1953		1954		1953		1954		1953		1954	
	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2
Chinese Spring	42.0	39.8	50.8	48.5	41.6	40.4	48.0	48.5	41.2	40.6	49.5	48.7
1	43.0	41.2	49.8	50.6	43.2	41.6	49.4	50.8	40.6	41.8	48.8	48.5
2	41.6	41.8	47.5	46.9	40.8	41.6	47.5	48.3	37.2	40.0	49.0	47.8
3	41.0	39.6	45.1	44.3	40.8	40.6	47.4	50.4	41.8	41.8	50.4	49.6
4	40.2	42.4	47.0	49.8	38.8	42.2	48.3	48.8	41.2	39.8	49.0	49.3
5	41.4	40.4	46.5	47.4	43.4	44.6	48.8	50.1	41.6	37.0	48.4	47.1
6	41.2	40.0	48.5	48.4	41.8	41.0	47.1	47.6	43.0	41.8	53.4	52.9
7	39.0	39.6	41.1	45.0	41.0	41.4	47.1	50.0	41.0	39.4	46.6	47.0
8	41.0	38.0	42.6	44.9	40.0	38.6	44.6	45.5	40.2	37.8	44.6	45.2
9	39.4	40.2	44.8	41.9	42.0	42.6	46.6	47.9	39.4	39.6	49.7	50.7
10	42.2	40.0	48.3	44.3	41.6	42.4	49.9	48.0	40.6	40.2	51.2	48.4
11	41.0	39.8	51.5	48.3	43.6	42.0	49.9	52.5	39.8	41.8	52.2	53.1
12	41.0	41.0	42.2	41.6	41.2	41.8	46.1	46.5	41.8	43.0	49.0	50.9
15	41.0	38.8	48.1	46.6	41.0	40.2	47.1	47.4	41.4	41.0	50.1	48.6
16	43.0	40.8	49.3	50.0	41.6	39.4	49.6	48.5	40.0	40.2	47.6	48.3
19	41.8	41.0	48.1	48.8	43.6	45.0	49.8	50.1	42.8	40.2	51.5	50.3
20	42.0	39.8	50.0	49.4	40.0	39.2	46.1	48.8	40.8	40.8	50.2	48.6
21	42.2	43.2	49.6	47.1	44.8	43.4	48.9	50.8	42.8	39.2	49.4	49.6

Table 14 (continued)

Analysis of Variance

Source of variation	df	ss	ms	F	5%	1%
Total	215	3652.25				
Reps	1	2.96	2.96			
Years	1	2810.17	2810.17			
Varieties	2	50.70	25.35			
Years x Varieties	2	59.96	29.98			
Error (1)	5	20.06	4.01			
Lines	17	241.97	14.23			
Lines x Years	17	79.84	4.70	0.85	1.94	2.55
Lines x Varieties	34	188.12	5.53	2.75xx	1.77	2.26
Lines x Varieties x Years	34	68.30	2.01	1.57x	1.54	1.85
Error (2)	102	130.17	1.28			

	LxYxV	LxV	L
L.S.D. 5% level	-2.24	-2.03	1.95
1% level	-2.97	-2.73	2.62

Table 15

Computation of lines x varieties interaction of plant height from composite of 3 sets of substitution lines in 1953.

Chromosome tested	Hope				Ave.	Timstein				Ave.	Thatcher				Ave.
Chinese Spring	42.0	39.8	41.6	41.0	41.10	41.6	40.4	41.8	41.2	41.25	41.2	40.6	41.4	40.8	41.00
1	43.0	41.2	42.0	43.2	42.35	43.2	41.6	40.6	40.8	41.55	40.6	41.8	42.0	39.4	40.95
2	41.6	41.8	41.8	39.0	41.05	40.8	41.6	40.8	43.0	41.55	37.2	40.0	41.4	39.6	39.55
3	41.0	39.6	39.4	39.2	39.80	40.8	40.6	39.8	40.0	40.30	41.8	41.8	41.4	41.8	41.70
4	40.2	42.4	42.2	41.0	41.45	38.8	42.2	40.8	39.8	40.40	41.2	39.8	40.6	39.0	40.12
5	41.4	40.4	40.4	40.4	40.65	43.4	44.6	43.4	41.6	43.25	41.6	37.0	40.6	40.2	39.85
6	41.2	40.0	42.0	40.4	40.90	41.8	41.0	41.2	41.4	41.35	43.0	41.8	44.8	41.4	42.75
7	39.0	39.6	40.0	40.0	39.65	41.0	41.4	42.4	40.6	41.35	41.0	39.4	40.6	39.8	40.20
8	41.0	38.0	39.2	39.6	39.45	40.0	38.6	37.6	37.8	38.50	40.2	37.8	39.0	38.2	38.80
9	39.4	40.2	38.6	36.8	38.75	42.0	42.6	41.4	41.4	41.85	39.4	39.6	37.0	39.2	38.80
10	42.2	40.0	42.2	40.0	41.10	41.6	42.4	38.4	40.8	40.80	40.6	40.2	41.2	40.7	40.68
11	41.0	39.8	40.6	40.6	40.50	43.6	42.0	41.2	42.8	42.40	39.8	41.8	42.4	40.6	41.15
12	41.0	41.0	43.2	39.6	41.20	41.2	41.8	39.6	39.0	40.40	41.8	43.0	43.0	42.0	42.45
15	41.0	38.8	41.2	39.6	40.15	41.0	40.2	37.8	41.4	40.10	41.4	41.0	42.8	40.4	41.40
16	43.0	40.8	42.0	41.0	41.70	41.6	39.4	40.4	40.6	40.50	40.0	40.2	41.6	39.6	40.32
19	41.8	41.0	45.0	42.4	42.55	43.6	45.0	42.4	41.6	43.15	42.8	40.2	42.6	40.2	41.45
20	42.0	39.8	40.8	41.2	40.95	40.0	39.2	40.0	39.2	39.60	40.8	40.8	41.6	39.6	40.70
21	42.2	43.2	44.2	40.4	42.50	44.8	43.4	41.0	43.2	43.10	42.8	39.2	41.6	40.4	41.00

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	215					
Reps	3	25.31	8.437			
Varieties	2	8.25	4.135			
Error (1)	6	28.10	4.683			
Lines	17	137.80	8.106			
Lines x Varieties	34	126.45	3.719	3.625xx	1.51	1.79
Error (2)	153	156.99	1.026			

L.S.D. 5% level = 0.716 x 1.978 = 1.42
1% level = 0.716 x 2.614 = 1.87

Table 16

Computation of lines x varieties interaction of plant height from composite of 3 sets of substitution lines in 1954.

Chromosome tested	Hope		Ave.	Thatcher		Ave.	Timstein		Ave.
Chinese Spring	50.8	48.5	49.7	49.5	48.7	49.1	48.0	48.5	48.3
1	49.8	50.6	50.2	48.8	48.5	48.7	49.4	50.8	50.1
2	47.5	46.9	47.2	49.0	47.8	48.4	47.5	48.3	47.9
3	45.1	44.3	44.7	50.4	49.6	50.0	47.4	50.4	48.9
4	47.0	49.8	48.4	49.0	49.3	49.2	48.3	48.8	48.6
5	46.5	47.4	47.0	48.4	47.1	47.8	48.8	50.1	49.5
6	48.5	48.4	48.5	53.4	52.9	53.2	47.1	47.6	47.4
7	41.1	45.0	43.1	46.6	47.0	46.8	47.1	50.0	48.6
8	42.6	44.9	43.8	44.6	45.2	44.9	44.6	45.5	45.1
9	44.8	41.9	43.4	49.7	50.7	50.2	46.6	47.9	47.3
10	48.3	44.3	46.3	51.2	48.4	49.8	49.9	48.0	49.0
11	51.5	48.3	49.9	52.2	53.1	52.7	49.9	52.5	51.2
12	42.2	41.6	41.9	49.0	50.9	50.0	46.1	46.5	42.3
15	48.1	46.6	47.4	50.1	48.6	49.4	47.1	47.4	47.3
16	49.3	50.0	49.7	47.6	48.3	48.0	49.6	48.5	49.1
18	49.0	51.0	40.0	49.3	49.3	49.3	46.6	48.8	47.8
19	48.1	48.8	48.5	51.5	50.3	50.9	49.8	50.1	50.0
20	50.0	49.4	49.7	50.2	48.6	49.4	46.1	48.8	47.5
21	49.6	47.1	48.4	49.4	49.6	49.5	48.9	50.8	49.9

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	113					
Reps	1	0.79	0.79			
Varieties	2	82.80	41.40			
Error (1)	2	11.87	5.94			
Lines	18	259.71	14.43			
Lines x varieties	36	195.47	5.43	3.69xx	1.64	2.01
Error (2)	54	68.81	1.47			

L.S.D. 5% level = 1.2 x 2.005 = 2.40
1% level = 1.2 x 2.671 = 3.21

TABLE 17

Chinese Spring lines with substituted Thatcher chromosomes.

Chromosome tested	Height in inches. Series 1	Series 2	Series 3	Series 4	Total	1952 Average
Thatcher	44	44	44	44	176	44
Chinese Spring	42	45	44	44	175	43.75
1	45	45	45	45	180	45
2	44	43	43	43	173	43.25
3	45	45	45	45	180	45
4	45	43	42	45	175	43.75
5	44	44	43	43	174	43.5
6	46	45	44	44	179	44.75
7	43	44	43	43	173	43.25
8	40	42	38	41	161	40.25
9	43	42	41	41	167	41.75
10	43	44	43	44	174	43.50
11	47	47	44	45	183	45.75
12	45	45	46	41	177	44.25
15	44	44	43	44	175	43.75
16	41	39	38	40	158	39.50
17	46	45	45	46	182	45.50
19	44	44	44	45	177	44.25
20	42	43	44	44	173	43.25
21	42	43	43	42	170	42.50

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	252				
Reps	3	6.	2.00	2.04xx		
Lines	19	190	10.00	10.2		
Error	57	56	0.98 (1 approx.)			

L.S.D. (1) 5% point - t.05 $x\sqrt{\frac{2x1}{4}}$ = 2.002 x .7 = 1.4014

(11) 1% point - t.01 $x\sqrt{\frac{2x}{4}}$ = 2.666 x .7 = 1.8662

TABLE 18

Chinese Spring lines with substituted Thatcher chromosomes

Height in inches 1953

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Total	Average
Thatcher	39.6	39.0	41.8	38.8	159.2	39.8
Chinese Spring	41.2	40.6	41.4	40.8	164.0	41.0
1	40.6	41.8	42.0	39.4	163.8	40.9
2	40.3	40.0	41.4	39.6	161.3	40.3
3	41.8	41.8	41.4	41.8	166.8	41.7
4	41.2	39.8	40.6	39.0	160.6	40.1
5	41.6	40.0	40.6	40.2	162.4	40.6
6	43.0	41.8	44.8	41.4	171.0	42.7
7	41.0	39.4	40.6	39.8	160.8	40.2
8	40.2	37.8	39.0	38.2	155.2	38.8
9	40.8	40.4	41.0	41.4	163.6	40.9
10	40.6	40.2	41.2	40.7	162.7	40.7
11	43.8	41.2	42.4	40.8	168.2	42.0
12	41.8	43.0	43.0	42.0	169.8	42.4
13	41.4	41.0	41.4	41.0	164.8	41.2
15	41.4	41.0	42.8	40.4	165.6	41.4
16	40.0	40.2	41.6	39.6	161.4	40.3
17	41.0	40.6	43.6	40.2	165.4	41.3
18	43.8	41.4	41.2	41.0	167.4	41.8
19	42.8	40.2	42.6	40.2	165.8	41.4
20	40.8	40.8	41.6	39.6	162.8	40.7
21	42.8	39.2	41.6	40.4	164.0	41.0

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	87	137.1				
reps	3	31.7	10.57	17.62xx	2.75	4.11
lines	21	67.6	3.22	5.37	1.73	2.17
error	63	37.8	0.60			

L.S.D. 5% point = 0.543 x 1.999 = 1.085
1% point = 0.543 x 2.657 = 1.442

TABLE 19

Chinese Spring lines with substituted Thatcher chromosomes.

1954

Chromosome tested	Height in inches Series 1	Series 2	Total	Average
Thatcher	42.4	42.6	85.0	42.5
Chinese Spring	49.5	48.7	98.2	49.1
1	48.8	48.5	97.3	48.7
2	49.0	47.8	96.8	48.4
3	50.4	49.6	100.0	50.0
4	49.0	49.3	98.3	49.2
5	48.4	47.1	95.5	47.8
6	53.4	52.9	106.3	52.3
7	46.6	47.0	93.6	46.8
8	44.6	45.2	89.8	44.9
9	49.7	50.7	100.4	50.2
10	51.2	48.4	99.6	49.8
11	52.5	53.1	105.3	52.7
12	49.0	50.9	99.9	50.0
13	50.2	49.5	99.7	49.9
15	50.1	48.6	98.7	49.4
16	47.6	48.3	95.9	48.0
18	49.3	49.3	98.6	49.3
19	51.5	50.3	101.8	50.9
20	50.2	48.6	98.8	49.4
21	49.4	50.6	100.0	50.0
22(10)	49.6	48.8	98.4	49.2
23(16)	47.8	47.0	94.8	47.4
24(19)	49.4	49.6	99.0	49.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	47	2346.5				
reps	1	9.9				
lines	23	2203.2	95.8	16.5	2.01	2.72
error	23	133.4	5.8			

L.S.D. 5% point - 2.07 x 2.4 = 4.97
1% point - 2.81 x 2.4 = 6.74

TABLE 20

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Height in inches Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Hope	41.8	41.4	44.2	43.4	170.8	42.7
Chinese Spring	42.0	39.8	41.6	41.0	164.4	41.1
1	43.0	41.2	42.0	43.2	169.4	42.3
2	41.6	41.8	41.8	39.0	164.2	41.0
3	41.0	39.6	39.4	39.2	159.2	40.0
4	40.2	42.4	42.2	41.0	165.8	41.4
5	41.4	40.4	40.4	40.4	162.6	40.6
6	41.2	40.0	42.0	40.4	163.6	40.9
7	39.0	39.6	40.0	40.0	158.6	39.6
8	41.0	38.0	39.2	39.6	157.8	39.4
9	39.4	40.2	38.6(B)	36.8	155.0	38.7
10	42.2	40.0	42.2	40.0	164.4	41.1
11	41.0	39.8	40.6	40.6	162.0	40.5
12	41.0	41.0	43.2	39.6	164.8	41.2
13						
15	41.0	38.8	41.2	39.6	160.6	40.1
16	43.0	40.8	42.0	41.0	166.8	41.7
17	41.2	39.6	41.8	41.0	163.6	40.9
18						42.0
19	41.8	41.0	45.0	42.4	170.2	42.5
20	42.0	39.8	40.8	41.2	163.8	41.6
21	42.2	43.2	44.2	40.4	170.0	42.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	6560				
Reps	3	21	7.0			
Lines	20	6503	325.1	355^{xx}	1.75	2.20
Error	60	56	0.9333			

L.S.D. (1) 5% point - t.05 - .683 x 2.0 = 1.366

(11)1% point - t.01 - .683 x 2.66 = 1.81678

TABLE 21

Chinese Spring lines with substituted Hope chromosomes.

Chromosome tested	Height in inches Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Hope	47.6	47.3	46.4	46.9	188.2	47.1
Chinese Spring	50.8	48.5	48.3	49.5	197.1	49.3
1	49.8	50.6	49.6	49.9	199.9	50.0
2	47.5	46.9	46.3	46.5	187.2	46.7
3	45.1	44.3	44.3	44.7	178.4	44.6
4	47.0	49.8	47.9	49.0	193.7	48.4
5	46.5	47.4	46.9	47.6	188.4	47.1
6	48.5	48.4	47.7	48.5	193.1	48.4
7	41.1	45.0	43.4	43.6	173.1	43.3
8	42.6	44.9	43.2	43.4	174.1	43.5
9	44.8	41.9	43.4	43.2	173.3	43.3
10	48.3	44.3	46.3	45.5	184.4	46.0
11	51.5	48.3	48.3	48.5	196.6	49.2
12	42.2	41.6	44.4	45.3	173.5	43.4
15	48.1	46.6	46.4	48.4	189.5	47.4
16	49.3	50.0	50.0	52.9	202.2	50.6
17	49.1	49.1	48.4	50.2	196.8	49.2
18	49.0	51.0	49.9	52.2	202.1	50.3
19	48.1	48.8	50.0	50.6	197.5	50.1
20	50.0	49.4	49.3	51.0	199.7	49.9
21	49.6	47.1	48.0	48.9	193.6	49.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	5765.8				
Reps	3	89.7				
Lines	20	4967.6	248.40	21.03	1.75	2.20
Error	60	708.5	11.81			

L.S.D. 5% point - 2.43 x 2.00 = 4.86
1% point - 2.43 x 2.66 = 6.46

TABLE 22

Chinese Spring lines with substituted Timstein chromosomes

Height in inches

1953

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Total	Average
Timstein	37.6	36.8	34.4	36.0	144.8	36.2
Chinese Spring	41.6	40.4	41.8	41.2	165.0	41.2
1	43.2	41.6	40.6	40.8	166.2	41.5
2	40.8	41.6	40.8	43.0	166.2	41.5
3	40.8	40.6	39.8	40.0	161.2	40.3
4	38.8(B)	42.2	40.8	39.8	161.6	40.4
5	43.4	44.6	43.4	41.6	173.0	43.2
6	41.8	41.0	41.2	41.4	165.4	41.3
7	41.0	41.4	42.4	40.6	165.4	41.3
8	40.0	38.6	37.6	37.8	154.0	38.5
9	42.0	42.6	41.4	41.4	167.4	41.8
10	41.6	42.4	38.4	40.8	163.2	40.8
11	43.6	42.0	41.2	42.8	169.6	42.4
12	41.2	41.8	39.6	39.0	161.6	40.4
15	41.0	40.2	37.8	41.4	160.4	40.1
16	41.6	39.4	40.4	40.6	162.0	40.5
17	41.8	40.0	39.8	40.2	161.8	40.8
18	41.4	40.6	40.8	40.2	163.0	40.7
19	43.6	45.0	42.4	41.6	172.6	43.4
20	40.0	39.2	40.0	39.2	158.4	39.6
21	44.8	43.4	41.0	43.2	172.4	43.1

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	318.0				
Reps	3	20.0	6.66	4.3		
Lines	20	205.6	10.28	6.6xx	1.75	2.20
Error	60	92.4	1.54			

L.S.D. 5% point - 2.0 x .88 = 1.76

1% point - 2.66 x .88 = 2.3408

TABLE 23

Chinese Spring lines with substituted Timstein chromosomes.

1954

Chromosome tested	Height in inches Series 1	Series 2	Series 3	Series 4	Total	Average
Timstein	35.6	35.5	35.5	35.0	141.6	35.4
Chinese Spring	48.0	48.5	49.5	48.8	194.8	48.7
1	49.4	50.8	48.7	52.3	201.2	50.3
2	47.5	48.3	47.8	47.5	191.1	49.3
3	47.4	50.4	48.2	46.2	192.2	48.1
4	48.3	48.8	51.0	51.0	199.1	49.8
5	48.8	50.1	48.1	48.5	195.5	50.4
6	47.1	47.6	48.5	48.0	191.2	47.8
7	47.1	50.0	46.9	50.1	194.1	48.5
8	44.6	45.5	44.2	45.1	179.4	44.9
9	46.6	47.9	46.1	47.2	187.8	47.5
10	49.9	48.0	48.2	48.5	194.6	48.7
11	49.9	52.5	48.9	51.2	202.5	50.6
12	46.1	46.5	44.5	45.7	182.8	47.6
15	47.1	47.4	46.7	47.2	188.4	48.1
16	49.6	48.5	48.6	50.0	196.7	49.2
17	50.1	50.3	49.1	52.5	202.0	50.5
18	46.6	48.8	49.5	46.7	191.6	47.9
19	49.8	50.1	49.7	52.5	202.1	50.5
20	46.1	48.8	47.4	46.5	188.8	46.7
21	48.9	50.8	51.1	51.4	202.2	50.6

Analysis of Variance

Source	ss	df	ms	F	5%	1%
Total	83	9360.3				
Reps	3	145.7				
Lines	20	8558.8	427.94xx	39.2	1.75	2.20
Error	60	655.8	10.93			

L.S.D. - 5% point - 2.00 x 2.34 = 4.68

- 1% point - 2.66 x 2.34 = 6.22

Table 24

Computation of lines x years interaction of lodging scores from composite of 3 sets of substitution lines in 1953 and 1954.

	Thatcher				Hope				Timstein			
	1953'		1954'		1953'		1954'		1953'		1954'	
	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2
Chinese Spring	4.2	3.2	3.0	4.0	4.2	3.6	3.0	3.0	5.2	4.0	4.0	3.0
1	7.8	8.4	8.0	9.0	6.6	8.2	7.0	5.0	6.8	7.0	7.0	5.5
2	7.4	5.8	7.0	8.0	5.2	6.6	9.0	7.5	6.8	4.6	6.0	7.0
3	4.4	6.8	5.5	6.0	7.0	7.6	7.5	7.0	5.8	3.8	4.0	5.5
4	5.4	3.8	3.0	3.0	6.6	7.4	5.0	6.0	7.2	5.0	6.0	5.5
5	8.4	7.6	8.0	9.0	7.6	5.0	7.5	8.0	8.6	8.4	9.0	9.0
6	6.8	5.4	6.5	6.5	7.2	4.6	5.5	7.5	5.8	5.2	6.0	6.5
7	6.4	6.4	6.5	7.0	8.8	7.8	8.0	8.5	6.0	4.6	6.0	5.5
8	7.8	8.4	7.5	8.0	6.8	7.2	7.0	6.5	8.4	8.4	7.0	7.5
9	7.8	9.4	6.0	7.0	7.6	6.8	8.5	8.5	5.6	3.8	8.0	8.5
10	4.4	2.8	2.0	3.0	4.4	4.8	4.0	6.0	8.2	8.4	7.0	8.0
11	4.0	4.2	3.0	4.5	3.8	2.8	2.5	2.0	6.0	3.6	5.0	5.0
12	6.0	6.8	5.0	6.0	6.6	7.4	7.0	7.0	5.4	5.4	7.0	7.0
15	3.4	4.0	3.0	5.0	3.6	3.4	6.0	4.0	6.2	4.2	7.5	6.0
16	8.2	6.6	4.0	4.0	4.8	3.4	4.0	5.5	3.8	5.2	6.5	4.0
19	3.8	3.6	7.0	6.0	7.0	8.2	3.0	5.5	7.6	8.8	7.0	7.0
20	6.8	6.2	6.0	7.0	5.8	2.6	2.5	2.0	4.0	3.2	3.0	3.0
21	7.2	5.2	7.0	7.0	7.2	6.8	7.5	9.0	5.8	4.8	3.0	4.0

Table 24 (continued)

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	215	706.30				
Reps	1	0.73	0.73			
Varieties	2	0.26	0.13			
Years	1	0.07	0.07			
Years x Varieties	2	0.96	0.48			
Error (1)	5	13.94	2.79			
Lines	17	325.70	19.16			
LxY	17	28.32	1.67	0.87	1.94	2.55
LxV	34	202.29	5.95	3.08*	1.77	2.26
LxYxV	34	65.45	1.93*	2.88**	1.54	1.85
Error (2)	102	68.58	0.67			

		LxYxV	LxV	L
L.S.D.	5% level	1.63	1.99	2.02
	1% level	2.15	2.67	2.72

Table 25

Computation of lines x varieties interaction of lodging scores from composite of 3 sets of substitution lines in 1953.

Chromosome tested	Hope				Ave.	Thatcher				Ave.	Timstein				Ave.
Chinese Spring	4.2	3.6	5.6	4.0	4.4	4.2	3.2	3.8	4.6	3.95	5.2	4.0	5.2	6.2	5.15
1	6.6	8.2	6.6	7.6	7.3	7.8	8.4	7.8	8.8	8.20	6.8	7.0	8.0	6.6	7.10
2	5.2	6.6	8.2	8.4	7.1	7.4	5.8	7.4	7.4	7.00	6.8	4.6	6.6	4.2	5.55
3	7.0	7.6	7.6	7.6	7.5	4.4	6.8	7.8	6.0	6.25	5.8	3.8	5.8	7.0	5.60
4	6.6	7.4	7.4	4.8	6.6	5.4	3.8	6.8	5.8	5.45	7.2	5.0	6.6	7.4	6.55
5	7.6	5.0	8.0	7.2	7.0	8.4	7.6	7.4	7.4	7.70	8.6	8.4	7.2	5.4	7.40
6	7.2	4.6	6.8	6.2	6.2	6.8	5.4	6.4	5.2	5.95	5.8	5.2	6.8	5.8	5.90
7	8.8	7.8	4.6	7.2	7.1	6.4	6.4	5.8	6.6	6.30	6.0	4.6	5.8	6.2	5.65
8	6.8	7.2	7.6	8.0	7.4	7.8	8.4	7.4	8.4	8.00	8.4	8.4	8.6	8.8	8.55
9	7.6	6.8	7.6	7.0	7.3	7.8	9.0	7.6	7.8	8.05	5.6	3.8	5.2	4.0	4.65
10	4.4	4.8	6.8	5.8	5.5	4.4	2.8	4.4	5.8	4.35	8.2	8.4	8.2	8.8	8.40
11	3.8	2.8	2.8	4.2	3.4	4.0	4.2	4.2	4.4	4.20	6.0	3.6	5.6	6.2	5.35
12	6.6	7.4	6.8	7.4	7.1	6.0	6.8	4.8	6.8	6.10	5.4	5.4	5.2	6.0	5.50
15	3.6	3.4	5.2	5.4	4.4	3.4	4.0	3.2	5.0	3.90	6.2	4.2	6.8	5.4	5.65
16	4.8	3.4	4.4	7.2	5.0	8.2	6.6	5.2	6.4	6.60	3.8	5.2	7.6	6.8	5.85
19	7.0	8.2	8.0	8.4	7.9	3.8	3.6	6.0	5.0	4.60	7.6	8.8	8.6	8.0	8.25
20	5.8	2.6	4.4	6.0	4.7	6.8	6.2	5.0	5.8	5.95	4.0	3.2	5.8	5.6	4.65
21	7.2	6.8	5.8	6.6	6.6	7.2	5.2	7.8	5.8	6.50	5.8	4.8	5.8	4.4	5.20

Analysis of Variance

Source	df	ss	ms	F	0.05	0.01
Total	215					
Reps	3	16.89	5.630			
Varieties	2	1.02	0.510			
Error (1)	6	5.00	0.833			
Lines	17	209.20	12.306			
Lines x varieties	34	155.89	4.505	5.111[xx]	1.51	1.79
Error (2)	153	137.24	0.897			

L.S.D. 5% level - .67 x 2.007 = 1.34
1% level - .67 x 2.676 = 1.80

Table 26

Computation of lines x varieties interaction of lodging scores from composite of 3 sets of substitution lines in 1954.

Chromosome tested	Hope		Ave.	Timstein		Ave.	Thatcher		Ave.
Chinese Spring	3.0	3.0	3.0	4.0	3.0	3.5	3.0	4.0	3.5
1	7.0	5.0	6.0	7.0	5.5	6.25	8.0	9.0	8.5
2	9.0	7.5	8.25	6.0	7.0	6.5	7.0	8.0	7.5
3	7.5	7.0	7.25	4.0	5.5	4.75	5.5	6.0	5.75
4	5.0	6.0	5.5	6.0	5.5	5.75	3.0	3.0	3.0
5	7.5	8.0	7.75	9.0	9.0	9.0	8.0	9.0	8.5
6	5.5	7.5	6.5	6.0	6.5	6.25	6.5	6.5	6.5
7	8.0	8.5	8.25	6.0	5.5	5.75	6.5	7.0	6.75
8	7.0	6.5	6.75	7.0	7.5	7.25	7.5	8.0	7.75
9	8.5	8.5	8.5	8.0	8.5	8.25	6.0	7.0	6.5
10	4.0	6.0	5.0	7.0	8.0	7.5	2.0	3.0	2.5
11	2.5	2.0	2.25	5.0	5.0	5.0	3.0	4.5	3.75
12	7.0	7.0	7.0	7.0	7.0	7.0	5.0	6.0	5.5
15	6.0	4.0	5.0	7.5	6.0	6.75	3.0	5.0	4.0
16	4.0	5.5	4.75	6.5	4.0	5.25	4.0	4.0	4.0
19	3.0	5.5	4.25	7.0	7.0	7.0	7.0	6.0	6.5
20	2.5	2.0	2.25	3.0	3.0	3.0	6.0	7.0	6.5
21	7.5	9.0	8.25	3.0	4.0	3.5	7.0	7.0	7.0

Analysis of Variance

Source	df	ss	ms	F	0.05	0.01
Total	107					
Reps	1	1.95	1.950			
Varieties	2	1.01	0.505			
Error (1)	2	2.56	1.280			
Lines	17	217.69	12.805			
Lines x varieties	34	137.66	4.049	11.25^{xx}	1.67	2.05
Error (2)	51	18.36	0.360			

L.S.D. 5% level - 2.007 x .6 = 1.20
1% level - 2.676 x .6 = 1.61

Table 27

Chinese Spring lines with substituted Thatcher chromosomes.

Lodging 1952

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Average
Thatcher	10.0	10.0	10.0	10.0	10.0
Chinese Spring	4.5	5.0	4.0	4.5	4.5
1	9.5	8.5	9.0	9.0	9.0
2	8.0	9.0	6.5	8.5	8.0
3	6.5	7.0	7.5	7.0	7.0
4	6.0	5.0	6.5	6.5	6.0
5	7.0	6.5	7.5	7.0	7.0
6	7.5	7.0	6.5	7.0	7.0
7	7.0	7.0	7.0	7.0	7.0
8	9.5	8.5	8.0	8.0	8.5
9	7.5	8.5	8.0	8.0	8.0
10	5.5	4.5	6.0	6.0	5.5
11	4.0	5.0	4.5	4.5	4.5
12	6.0	6.5	6.0	5.5	6.0
13					7.0
15	5.5	5.5	5.5	5.5	5.5
16	6.0	6.5	5.5	6.0	6.0
17	4.0	4.5	5.5	4.0	4.5
19	6.0	6.0	6.0	6.0	6.0
20	6.5	6.0	6.0	5.5	6.0
21	6.0	6.5	7.0	6.5	6.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	186.75				
Reps	3	0.025	1			
Lines	19	146.75	7.72	11.01	1.77	2.25
Error	57	39.98	0.701			

L.S.D. (1) 5% - 2.002 x 0.592 = 1.185185 or 1.19
(11) 1% - 2.666 x 0.592 = 1.578272 or 1.58

Table 28

Chinese Spring Lines with substituted Thatcher chromosomes

Chromosome tested	Lodging Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Thatcher	9.2	9.6	9.8	9.8	38.4	9.60
Chinese Spring	4.2	3.2	3.8	4.6	15.8-	3.95
1	7.8	8.4	7.8	8.8	32.8	8.20
2	7.4	5.8	7.4	7.4	28.0	7.00
3	4.4	6.8	7.8	6.0	25.0	6.25
4	5.4	3.8	6.8	5.8	21.8	5.45
5	8.4	7.6	7.4	7.4	30.8	7.70
6	6.8	5.4	6.4	5.2	23.8	5.95
7	6.4	6.4	5.8	6.6	25.2	6.30
8	7.8	8.4	7.4	8.4	32.0	8.00
9	7.8	9.0	7.6	7.8	31.2	7.80
10	4.4	2.8	4.4	5.8	17.4	4.35
11	4.0	4.2	4.2	4.4	16.8	4.20
12	6.0	6.8	4.8	6.8	24.4	6.10
13	6.0	7.0	6.6	5.2	24.8	6.20
15	3.4	4.0	3.2	5.0	15.6	3.90
16	8.2	6.6	5.2	6.4	26.4	6.60
17	3.0	4.0	3.4	4.0	14.4	3.60
18	4.4	3.6	4.4	5.8	18.2	4.55
19	3.8	3.6	6.0	5.0	18.4	4.60
20	6.8	6.2	5.0	5.8	23.8	5.95
21	7.2	5.2	7.8	5.8	26.0	6.50

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	87	264.8				
Reps	3	2.5	0.833	1.18		
Lines	21	217.7	10.37	14.65	1.73	2.17
Error	63	44.6	0.708			

L.S.D. 5% point - .595 x 1.999 = 1.19
1% point - .595 x 2.657 = 1.58

Table 29

Chinese Spring lines with substituted Thatcher chromosomes

1954

Chromosome tested	Lodging Series 1	Series 2	Total	Average
Thatcher	9.5	10.0	19.5	9.75
Chinese Spring	3.0	4.0	7.0	3.5
1	8	9	17	8.5
2	7	8	15	7.5
3	5.5	6	11.5	5.75
4	3	3	3.0	3.0
5	8	9	17.0	8.5
6	6.5	6.5	13.0	6.5
7	6.5	7	13.5	6.75
8	7.5	8	15.5	7.75
9	6	7	13.0	6.5
10	2	3	5.0	2.5
11	3	4.5	7.5	3.75
12	5	6	11.0	5.5
13	late heading - impossible to compare			
15	3	5	8.0	4.0
16	4	4	8.0	4.0
18	late heading - impossible to compare			
19	7	6	13.0	6.5
20	6	7	13.0	6.5
21	7	7	14.0	7.0
22(10)	2	2	4.0	2.0
23(16)	5	4	9.0	4.5
24(10)	6	5	11.0	5.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	47	3130.0				
Lines	23	3038.8	132.12	44.5xx	2.01	2.72
Reps	1	23.0				
Error	23	68.2	2.97	1.73		

L.S.D. - 5% point - 1.73 x 2.07 = 3.58

1% point - 1.73 x 2.81 = 4.86

Table 30

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Lodging Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Hope	8.8	9.8	8.0	9.8	36.4	9.1
Chinese Spring	4.2	3.6	5.6	4.0	17.4	4.35
1	6.6	8.2	4.6	7.6	27.0	6.8
2	5.2	6.6	8.2	8.4	28.4	7.1
3	7.0	7.6	7.6	7.6	29.8	7.45
4	6.6	7.4	7.4	4.8	26.2	6.55
5	7.6	5.0	8.0	7.2	27.8	6.95
6	7.2	4.6	6.8	6.2	24.8	6.2
7	8.8	7.8	4.6	7.2	28.4	7.1
8	6.8	7.2	7.6	8.0	29.6	7.4
9	7.6	6.8	7.6	7.0	29.0	7.25
10	4.4	4.8	6.8	5.8	21.8	5.45
11	3.8	2.8	2.8	4.2	13.6	3.4
12	6.6	7.4	6.8	7.4	28.2	7.05
15	3.6	3.4	5.2	5.4	17.6	4.4
16	4.8	3.4	4.4	7.2	19.8	4.95
17	3.4	6.6	6.0	5.8	21.8	5.45
19	7.0	8.2	8.0	8.4	31.6	7.9
20	5.8	2.6	4.4	6.0	18.8	4.7
21	7.2	6.8	5.8	6.6	26.4	6.6

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	228.40				
reps	3	5.61	1.87	0.67		
lines	19	152.46	8.02	2.90^{xx}	1.77	2.25
error	57	158.07	2.77			

L.S.D. (1) 5% - 1.17 x 2.002 = 2.34
(11) 1% - 1.17 x 2.666 = 3.12

Table 31

Chinese Spring lines with substituted Hope chromosomes.

Chromosome tested	Lodging Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Hope	9	10	10	9.5	38.5	9.6
Chinese Spring	3	3	4	4	14.0	3.5
1	7	5	6	6	24.0	6.0
2	9	7.5	9	7.5	33.0	8.3
3	7.5	7	8	8	30.5	7.6
4	5	6	5	5	21.0	5.3
5	7.5	8	6	7	28.5	7.1
6	5.5	7.5	7	7	27.0	6.8
7	8	8.5	8.5	8	33.0	8.3
8	7	6.5	6	6	25.5	6.4
9	8.5	8.5	8.5	8.5	34.0	8.5
10	4	6	5	6	21.0	5.3
11	2.5	2	4	2	10.5	2.6
12	7	7	8	8	30.0	7.5
15	6	4	3	6	19.0	4.8
16	4	5.5	4	6	19.5	4.9
17	7.5	5.5	7.5	7	27.5	6.9
18	5	5	5	5	20.0	5.0
19	3	5.5	4	6	18.5	4.6
20	2.5	2	3	3	10.5	2.6
21	7.5	9	8.5	8	33.0	8.3

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	3492.5				
Reps	3	13.7				
Lines	20	3098.1	154.9	24.4^{xx}	1.75	2.20
Error	60	380.7	6.35			

L.S.D. - t.05 - 2.00 x 1.79 = 3.58

t.01 - 2.66 x 1.79 = 4.76

Table 32

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Lodging Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Timstein	9.8	8.0	9.6	9.8	37.2	9.3
Chinese Spring	5.2	4.0	5.2	6.2	20.6	5.15
1	6.8	7.0	8.0	6.6	28.4	7.1
2	6.8	4.6	6.6	4.2	22.2	5.55
3	5.8	3.8	5.8	7.0	22.4	5.6
4	7.2	5.0	6.6	7.4	26.2	6.55
5	8.6	8.4	7.2	5.4	29.6	7.4
6	5.8	5.2	6.8	5.8	23.6	5.9
7	6.0	4.6	5.8	6.2	22.6	5.65
8	8.4	8.4	8.6	8.8	34.2	8.55
9	5.6	3.8	5.2	4.0	18.6	4.65
10	8.2	8.4	8.2	8.8	33.6	8.4
11	6.0	3.6	5.6	6.2	21.4	5.35
12	5.4	5.4	5.2	6.0	22.0	5.5
15	6.2	4.2	6.8	5.4	22.6	5.65
16	3.8	5.2	7.6	6.8	23.4	5.85
17	6.6	4.0	7.4	6.2	24.2	6.05
18	3.8	7.0	7.0	5.6	23.4	5.85
19	7.6	8.8	8.6	8.0	33.0	8.25
20	4.0	3.2	5.8	5.6	18.6	4.65
21	5.8	4.8	5.8	4.4	20.8	5.2

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	214.52				
Reps	3	16.71	5.57	6.32xx		
Lines	20	144.93	7.25	8.24xx	1.75	2.20
Error	60	52.88	0.881			

L.S.D. (1) 5% point - t.05 - 2.000 x .66 = 1.32

(11) 1% point - t.01 - 2.660 x .66 = 1.76

Table 33

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Lodging Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Timstein	10	10	10	10	40.0	10
Chinese Spring	4	3	3	4	14.0	3.5
1	7	5.5	7	8	27.5	6.9
2	6	7	7	7	27.0	6.8
3	4	5.5	6	5	20.5	5.1
4	6	5.5	7	7	25.5	6.4
5	9	9	7	8.5	33.5	8.4
6	6	6.5	6	6	24.5	6.1
7	6	5.5	6	6	23.5	5.9
8	7	7.5	7	9	30.5	7.6
9	8	8.5	8.5	9	34.0	8.5
10	7	8	7	7	29.0	7.3
11	5	5	6	6	22.0	5.5
12	7	7	6	8	28.0	7.0
15	7.5	6	7	7.5	28.0	7.0
16	6.5	4	4	5	19.5	4.9
17	5.5	7	6	6.5	25.0	6.3
18	6.5	7	7	7	27.5	6.9
19	7	7	7	9	30.0	7.5
20	3	3	4	4	14.0	3.5
21	3	4	4.5	4.5	16.0	4.0

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	2462.5				
Reps	3	53.9				
Lines	20	2148.1	107.4^{xx}	2.47	1.75	2.20
Error	60	260.5	4.34			

L.S.D. - 5% point - 1.47 x 2.00 = 2.94

1% point - 1.47 x 2.66 = 3.91

Table 34

Computation of lines x years interaction of spike density from composite of 3 sets of substitution lines in 1953 and 1954.

	Thatcher				Hope				Timstein			
	1953		1954		1953		1954		1953		1954	
Chromosome tested	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2	Rep 1	Rep 2
Chinese Spring	2.93	2.89	3.48	3.46	2.96	2.99	3.29	3.56	2.79	2.93	3.45	3.52
1	2.73	2.73	3.22	3.04	2.96	2.95	3.30	3.19	2.96	2.81	3.20	3.37
2	2.76	2.73	3.21	3.32	3.20	3.27	3.78	3.68	2.90	2.94	3.63	3.65
3	2.41	2.36	2.95	3.00	2.88	2.76	3.30	3.25	2.64	2.58	3.00	3.07
4	3.11	3.04	3.61	3.61	2.92	2.78	3.25	3.33	2.96	3.06	3.57	3.70
5	2.76	2.76	3.16	3.04	2.76	2.76	3.15	3.08	2.71	2.68	3.08	3.37
6	2.42	2.37	3.10	2.97	2.67	2.60	2.94	3.17	2.71	2.64	3.18	3.24
7	2.64	2.66	3.10	3.16	2.69	2.72	3.46	3.22	2.68	2.65	3.39	3.36
8	2.33	2.30	2.76	2.85	2.49	2.41	2.97	2.89	2.65	2.62	3.11	3.20
9	2.55	2.48	2.90	2.97	3.18	3.10	3.91	3.25	2.80	2.89	3.74	3.69
10	2.21	2.40	2.92	2.55	2.22	2.25	2.83	2.66	2.79	2.77	3.04	3.09
11	2.89	2.70	3.31	3.34	2.92	2.87	3.32	3.06	2.66	2.67	3.16	3.06
12	2.46	2.54	3.00	3.18	3.20	3.19	3.78	3.36	3.20	3.15	3.76	3.86
15	2.69	2.69	3.55	3.26	2.73	2.99	3.03	3.43	3.17	3.11	3.42	3.43
16	2.83	2.81	3.52	3.36	2.97	3.01	3.32	3.54	2.74	2.70	3.28	3.25
19	2.65	2.57	3.08	2.96	2.86	2.93	3.17	3.14	2.66	2.70	3.15	3.12
20	2.53	2.56	3.34	3.21	2.47	2.13	3.00	2.92	2.25	2.24	2.71	2.79
21	2.59	2.59	3.00	2.86	2.77	2.78	3.30	3.16	2.81	2.72	3.21	3.20

Table 34 (continued)

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	215	27.73				
Reps	1	0				
Varieties	2	1.11	0.55			
Years	1	13.28	13.28			
Y x V	2	0.04	0.02			
Error (1)	5	0.10	0.02			
Lines	17	7.63	0.45			
L x Y	17	0.28	0.01647	0.15		
L x V	34	3.72	0.10941xx	10.63	1.54	1.84
L x Y x V	34	0.52	0.01529	1.49	1.54	1.84
Error (2)	102	1.05	0.01029			

		LxYxV	LxV	L
L.S.D.	5% level	0.1984 (0.2)	0.20	0.38
	1% level	0.2626 (0.26)	0.26	0.52

Table 35

Computation of lines x varieties interaction of spike density from composite of 3 sets of substitution lines in 1953.

Chromosome tested	Thatcher				Ave.	Hope				Ave.	Timstein				Ave.
Chinese Spring	2.79	2.89	2.93	2.89	2.88	2.79	2.99	2.96	2.99	2.93	2.99	2.92	2.79	2.93	2.91
1	2.58	2.77	2.73	2.73	2.70	2.83	3.04	2.96	2.95	2.95	2.81	2.71	2.96	2.81	2.82
2	2.71	2.62	2.76	2.73	2.71	3.36	3.27	3.20	3.27	3.28	2.93	3.07	2.90	2.94	2.96
3	2.30	2.30	2.41	2.36	2.34	2.72	2.79	2.88	2.76	2.79	2.45	2.51	2.64	2.58	2.54
4	3.08	3.04	3.11	3.04	3.07	2.77	2.95	2.92	2.78	2.86	2.92	2.92	2.96	3.06	2.97
5	2.65	2.60	2.76	2.76	2.69	2.68	2.70	2.76	2.76	2.73	2.64	2.62	2.71	2.68	2.66
6	2.33	2.39	2.42	2.37	2.38	2.53	2.70	2.67	2.60	2.63	2.66	2.56	2.71	2.64	2.64
7	2.66	2.54	2.64	2.66	2.63	2.59	2.84	2.69	2.72	2.71	2.79	2.62	2.68	2.65	2.69
8	2.26	2.32	2.33	2.30	2.30	2.36	2.38	2.49	2.41	2.41	2.68	2.56	2.65	2.62	2.63
9	2.48	2.56	2.55	2.48	2.52	3.02	3.03	3.18	3.10	3.08	2.90	2.77	2.80	2.89	2.84
10	2.45	2.46	2.21	2.40	2.38	2.18	2.22	2.22	2.25	2.22	2.68	2.70	2.79	2.77	2.74
11	2.71	2.80	2.89	2.70	2.78	2.83	2.93	2.92	2.87	2.89	2.68	2.59	2.66	2.67	2.65
12	2.46	2.52	2.46	2.54	2.50	3.28	3.15	3.20	3.19	3.21	3.09	3.27	3.20	3.15	3.18
15	2.59	2.66	2.69	2.69	2.66	2.75	2.90	2.73	2.99	2.84	3.00	2.99	3.17	3.11	3.07
16	2.69	2.87	2.83	2.81	2.80	2.97	3.06	2.97	3.01	3.00	2.70	2.63	2.74	2.70	2.69
17	2.67	2.59	2.67	2.62	2.64	2.58	2.66	2.70	2.66	2.65	2.81	2.80	2.67	2.73	2.75
19	2.57	2.61	2.65	2.57	2.60	2.82	2.81	2.86	2.93	2.86	2.80	2.65	2.66	2.70	2.70
20	2.53	2.51	2.53	2.56	2.53	2.27	2.43	2.47	2.13	2.33	2.12	2.17	2.25	2.24	2.19
21	2.48	2.49	2.59	2.59	2.54	2.66	2.67	2.77	2.78	2.72	2.65	2.70	2.81	2.72	2.72

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	227					
Reps	3	.1	.0333			
Varieties	2	1.4	0.700			
Error (1)	6	0.0	00			
Lines	19	7.5	0.394			
Lines x varieties	38	3.9	0.102	23.18^{xx}	1.48	1.75
Error (2)	159	0.7	0.0044			

L.S.D. 5% level 1.978 x 0.0469 = 0.093
1% level 2.614 x 0.0469 = 0.123

Table 36

Computation of lines x varieties interaction of spike density from composite of 3 sets of substitution lines in 1954.

Chromosome tested	Hope		Timstein		Thatcher	
Chinese Spring	3.29	3.56	3.45	3.52	3.48	3.46
1	3.30	3.19	3.20	3.37	3.22	3.04
2	3.78	3.68	3.63	3.65	3.21	3.32
3	3.30	3.25	3.00	3.07	2.95	3.00
4	3.25	3.33	3.57	3.70	3.61	3.61
5	3.15	3.08	3.08	3.37	3.16	3.04
6	2.94	3.17	3.18	3.24	3.10	2.97
7	3.46	3.22	3.39	3.36	3.10	3.16
8	2.97	2.89	3.11	3.20	2.76	2.85
9	3.91	3.25	3.74	3.69	2.90	2.97
10	2.83	2.66	3.04	3.09	2.92	2.55
11	3.32	3.06	3.16	3.06	3.31	3.34
12	3.78	3.36	3.76	3.86	3.00	3.18
15	3.03	3.43	3.42	3.43	3.55	3.26
16	3.32	3.54	3.28	3.25	3.52	3.36
18	3.37	3.35	3.47	3.60	3.40	3.31
19	3.17	3.14	3.15	3.12	3.08	2.96
20	3.00	2.92	2.71	2.79	3.34	3.21
21	3.30	3.16	3.21	3.20	3.00	2.86

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	113	8.1031				
Reps	1	0.0165	0.0165			
Varieties	2	0.4900	0.2450			
Error (1)	2	0.0861	0.4305			
Lines	18	4.4672	0.2481			
Lines x Varieties	36	2.2423	0.0622	3.49xx	1.69	2.10
Error (2)	54	0.9642	0.0178			

L.S.D. 5% level - 0.133 x 2.005 = 0.27
1% level - 0.133 x 2.671 = 0.36

Table 37

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Spike Length (centimeters) Series 1	Series 2	Series 3	Series 4	Total	1952 Average
Thatcher	7.3	6.7	7.0	7.0	28.0	7.0
Chinese Spring	6.7	6.4	6.3	6.6	26.0	6.5
1	6.8	7.1	6.5	6.8	27.2	6.8
2	6.5	6.3	6.1	6.3	25.2	6.3
3	6.4	6.7	7.0	6.7	26.8	6.7
4	5.5	5.7	5.4	5.4	22.0	5.5
5	6.2	6.4	6.0	6.2	24.8	6.2
6	6.7	7.0	6.5	6.6	26.8	6.7
7	5.8	6.0	5.7	5.8	23.3	5.8
8	6.0	5.7	5.8	5.8	23.3	5.8
9	7.1	7.0	6.8	6.8	27.7	6.9
10	7.4	7.1	7.0	6.9	28.4	7.1
11	7.1	7.1	6.9	7.3	28.4	7.1
12	5.9	5.7	5.6	6.0	23.2	5.8
15	6.3	6.1	6.0	6.0	24.4	6.1
16	4.6	4.9	5.2	4.9	19.6	4.9
17	6.9	6.7	7.1	6.7	27.4	6.9
19	6.6	6.4	6.7	6.3	26.0	6.5
20	5.8	6.2	6.0	6.0	24.0	6.0
21	7.4	7.6	7.5	7.4	29.9	7.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	328.98				
Reps	3	1.33	0.443			
Lines	20	308.58	15.43	48.52xx	1.75	2.20
Error	60	19.07	0.318			

L.S.D. (1) 5% point - t.05 - .4 x 2.0 = 0.80

(11) 1% point - t.01 - .2 x 2.66 = 1.064

Table 38

Chinese Spring lines with substituted Thatcher chromosomes.

Chromosome tested	No. of Spikelets Series 1	Series 2	Series 3	Series 4	Total	1952 Average
Thatcher	16.3	16.9	16.7	16.8	66.7	16.7
Chinese Spring	20.9	21.4	21.3	21.2	84.8	21.2
1	19.4	20.0	19.6	19.8	78.8	19.7
2	19.8	20.4	20.0	19.8	80.0	20.0
3	20.0	20.2	19.8	20.0	80.0	20.0
4	20.2	20.8	20.5	20.4	81.9	20.5
5	19.8	20.2	19.9	19.7	79.6	19.9
6	19.9	19.7	20.1	20.0	79.7	19.9
7	19.5	19.8	19.3	19.6	78.2	19.6
8	19.9	19.7	19.5	19.7	78.8	19.7
9	20.0	20.0	20.3	19.9	80.2	20.0
10	20.8	21.4	20.6	20.6	83.4	20.9
11	22.3	22.2	22.1	21.9	88.5	22.1
12	18.6	18.8	19.0	18.8	75.2	18.8
15	21.3	21.1	20.9	21.1	84.4	21.1
16	20.7	20.5	20.7	20.9	82.8	20.7
17	21.2	21.5	20.8	21.2	84.7	21.2
19	19.9	20.3	20.1	20.1	80.4	20.1
20	19.8	20.1	20.2	20.3	80.4	20.1
21	21.3	21.5	21.4	2.14	85.6	21.4

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	99.79				
Reps	3	0.66	0.22			
Lines	19	96.96	5.10	134xx	1.77	2.25
Error	57	2.17	.0380			

L.S.D. (1) 5% point - $t_{.05}$ - 2.002 x .14 = .28
(11) 1% point - $t_{.01}$ - 2.666 x .14 = .37

Table 39

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 3	Series 4	Total	1952 Average
Thatcher	2.23	2.52	2.39	2.40	9.54	2.36
Chinese Spring	3.12	3.34	3.38	3.21	13.05	3.26
1	2.85	2.82	3.02	2.91	11.60	2.90
2	3.05	3.24	3.28	3.14	12.71	3.18
3	3.13	3.01	2.83	2.99	11.96	2.99
4	3.67	3.65	3.80	3.78	14.90	3.73
5	3.19	3.16	3.32	3.02	12.69	3.17
6	2.97	2.81	3.09	3.03	11.90	2.98
7	3.36	3.30	3.39	3.38	13.43	3.36
8	3.32	3.46	3.36	3.40	13.54	3.39
9	2.82	2.86	2.99	2.93	11.60	2.90
10	2.81	3.01	2.94	2.99	11.75	2.94
11	3.14	3.13	3.20	3.00	12.47	3.12
12	3.15	3.30	3.39	3.13	12.97	3.24
15	3.38	3.46	3.48	3.52	13.84	3.46
16	4.50	4.18	3.98	4.27	16.93	4.23
17	3.07	3.21	2.93	3.16	12.37	3.09
18						
19	3.02	3.17	3.00	3.19	12.38	3.10
20	3.41	3.24	3.36	3.38	13.39	3.35
21	2.88	2.83	2.85	2.89	11.45	2.86

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	11.22				
Reps	3	0.02	0.007	0.636		
Lines	19	10.56	0.556	50.545xx	1.77	2.25
Error	57	0.64	0.011			

L.S.D. t.05 - 2.002 x 0.0742 = 0.149

t.01 - 2.666 x 0.0742 = 0.198

Table 40

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Spike Length (centimeters) Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Thatcher	8.7	8.3	8.4	8.5	33.9	8.5
Chinese Spring	7.6	7.3	7.2	7.3	29.4	7.4
1	7.9	7.4	7.5	7.5	30.3	7.6
2	7.5	7.8	7.4	7.5	30.2	7.6
3	8.3	8.2	7.9	8.1	32.5	8.1
4	6.6	6.7	6.6	6.7	26.6	6.7
5	7.4	7.5	7.1	7.1	29.1	7.3
6	8.2	8.0	7.9	8.1	32.2	8.1
7	7.1	7.4	7.2	7.1	28.8	7.2
8	8.0	7.9	7.8	7.9	31.6	7.9
9	9.0	8.8	8.8	9.0	35.6	8.9
10	8.5	8.4	8.4	8.6	33.9	8.4
11	7.9	7.6	7.4	7.9	30.8	7.7
12	8.0	7.9	8.0	7.8	31.7	7.9
13	7.6	7.9	7.4	7.4	30.3	7.6
15	8.1	7.9	7.8	7.8	31.6	7.9
16	7.2	6.8	6.9	6.9	27.8	7.0
17	7.8	8.0	7.8	7.9	31.5	7.9
18	7.3	7.2	7.3	7.0	28.8	7.2
19	8.4	8.2	8.1	8.4	33.1	8.3
20	7.9	7.9	7.9	7.8	31.5	7.9
21	9.0	8.9	8.6	8.6	35.1	8.8

Table 41

Chinese Spring lines with substituted Thatcher chromosomes

1953

Chromosome tested	Number of Spikelets Series 1	Series 2	Series 3	Series 4	Total	Average
Thatcher	16.6	16.6	16.6	16.5	66.3	16.6
Chinese Spring	21.2	21.1	21.1	21.1	84.5	21.1
1	20.4	20.5	20.5	20.5	81.9	20.5
2	20.3	20.4	20.4	20.5	81.6	20.4
3	19.1	18.9	19.0	19.1	76.1	19.0
4	20.3	20.4	20.5	20.4	81.6	20.4
5	19.6	19.5	19.6	19.6	78.3	19.6
6	19.1	19.1	19.1	19.2	76.5	19.1
7	18.9	18.8	19.0	18.9	75.6	18.9
8	18.1	18.3	18.2	18.2	72.8	18.2
9	22.3	22.5	22.4	22.3	89.5	22.4
10	20.8	20.7	20.6	20.6	82.7	20.7
11	21.4	21.3	21.4	21.3	85.4	21.4
12	19.7	19.9	19.7	19.8	79.1	19.8
13	22.6	22.7	22.7	22.6	90.6	22.7
15	21.0	21.0	21.0	21.0	84.0	21.0
16	19.4	19.5	19.5	19.4	77.8	19.5
17	20.8	20.7	20.8	20.7	83.0	20.8
18	22.6	22.7	22.6	22.7	90.6	22.7
19	21.6	21.4	21.5	21.6	86.1	21.5
20	20.0	19.8	20.1	20.0	79.9	20.0
21	22.3	22.2	22.3	22.3	89.1	22.3

Table 42

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 23	Series 4	Total	1953 Average
Thatcher	1.91	2.00	1.98	1.94	7.83	1.96
Chinese Spring	2.79	2.89	2.93	2.89	11.50	2.88
1	2.58	2.77	2.73	2.73	10.81	2.70
2	2.71	2.62	2.76	2.73	10.82	2.71
3	2.30	2.30	2.41	2.36	9.37	2.34
4	3.08	3.04	3.11	3.04	12.27	3.07
5	2.65	2.60	2.76	2.76	10.77	2.69
6	2.33	2.39	2.42	2.37	9.51	2.38
7	2.66	2.54	2.64	2.66	10.50	2.63
8	2.26	2.32	2.33	2.30	9.21	2.30
9	2.48	2.56	2.55	2.48	10.07	2.52
10	2.45	2.46	2.21	2.40	9.52	2.38
11	2.71	2.80	2.89	2.70	11.10	2.78
12	2.46	2.52	2.46	2.54	9.98	2.50
13	2.97	2.87	3.07	3.05	11.96	2.99
15	2.59	2.66	2.69	2.69	10.63	2.66
16	2.69	2.87	2.83	2.81	11.20	2.80
17	2.67	2.59	2.67	2.62	10.55	2.64
18	3.09	3.15	3.09	3.24	12.57	3.14
19	2.57	2.61	2.65	2.57	10.40	2.60
20	2.53	2.51	2.53	2.56	10.13	2.53
21	2.48	2.49	2.59	2.59	10,15	2.54

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	87	6.36				
Reps	3	0.04	0.01333	3.5		
Lines	21	6.08	0.2895	76.18	1.73	2.17
Error	63	0.24	0.0038			

L.S.D. 5% point - 0.044 x 1.999 = 0.088

1% point - 0.044 x 2.657 = 0.117

Table 43

Chinese Spring lines with substituted Thatcher chromosomes

1954

Chromosome tested	Spike Length Series 1	Series 2	Total	Average
Thatcher	7.1	6.7	13.8	6.90
Chinese Spring	6.2	6.5	12.7	6.35
1	6.5	6.7	13.2	6.60
2	6.6	5.9	12.5	6.25
3	6.6	6.4	13.0	6.50
4	5.9	5.7	11.6	5.80
5	6.0	6.2	12.2	6.10
6	6.9	6.9	13.8	6.90
7	6.2	5.8	12.0	6.00
8	7.0	6.6	13.6	6.80
9	7.4	7.5	14.9	7.45
10	7.5	8.0	15.5	7.75
11	6.8	6.8	13.6	6.80
12	6.5	6.2	12.7	6.35
13	7.1	7.0	14.1	7.05
15	6.1	6.5	12.6	6.30
16	6.0	6.1	12.1	6.05
18	6.5	6.8	13.3	6.65
19	7.1	7.2	14.3	7.15
20	6.5	6.2	12.7	6.35
21	7.5	7.5	15.0	7.50
22(10)	8.0	7.3	15.3	7.65
23(16)	6.1	6.3	12.4	6.20
24(19)	6.8	7.3	14.1	7.05

Analysis of Variance

Source	df	SS	ms	F	5%	1%
Total	47	15.09	0.01			
Reps	1	0.01	0.01	0.16		
Lines	23	13.73	0.597	10.119^{xx}	2.01	2.72
Error	23	1.35	0.059			

L.S.D. 5% point - 2.069 x 0.2429 = 0.5026

1% point - 2.807 x 0.2429 = 0.6818

Table 44

Chinese Spring lines with substituted Thatcher chromosomes

1954

Chromosome tested	Number of Spikelets Series 3	Series 4	Total	Average
Thatcher	16.3	15.5	31.8	15.9
Chinese Spring	21.6	22.5	44.1	22.15
1	20.9	20.4	41.3	20.65
2	21.2	19.6	40.8	20.4
3	19.5	19.3	38.8	19.4
4	21.3	21.3	42.6	21.3
5	19.0	18.9-	57.9	18.95
6	20.8	20.5	41.3	20.65
7	19.7	18.3	38.0	19.0
8	19.4	18.8	38.2	19.1
9	21.4	22.5	43.9	21.95
10	21.3	21.7	43.0	21.5
11	22.5	22.7	45.2	22.6
12	19.5	19.7	39.2	19.6
13	22.2	23.1	45.3	22.65
15	21.7	21.5	43.2	21.60
16	21.1	20.5	41.6	20.8
18	22.1	22.5	44.6	22.3
19	21.9	21.3	43.2	21.6
20	21.7	19.9	41.6	20.8
21	22.5	21.4	43.9	21.95
22(10)	21.3	21.3	42.6	21.3
23(16)	21.2	21.1	42.3	21.15
24(19)	22.0	21.3	43.3	21.65

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	47	114.22				
Reps	1	0.88	0.88	3.099		
Lines	23	106.80	4.643	16.349xx	2.01	2.72
Error	23	6.54	0.284			

L.S.D. 5% point = 2.000 x .532 = 1.06

1% point = 2.660 x .532 = 1.42

Table 45

Chinese Spring lines with substituted Thatcher chromosomes

1954

Chromosome tested	Spike Density Series 3	Series 4	Total	Average
Thatcher	2.30	2.31	4.61	2.31
Chinese Spring	3.48	3.46	6.94	3.47
1	3.22	3.04	6.26	3.13
2	3.21	3.32	6.53	3.27
3	2.95	3.00	5.95	2.98
4	3.61	3.61	7.22	3.61
5	3.16	3.04	6.20	3.10
6	3.10	2.97	6.07	3.04
7	3.10	3.16	6.26	3.13
8	2.76	2.85	5.61	2.81
9	2.90	2.97	5.87	2.94
10	2.92	2.55	5.47	2.74
11	3.31	3.34	6.65	3.33
12	3.00	3.18	6.18	3.09
13	3.13	3.30	6.43	3.22
15	3.55	3.26	6.81	3.41
16	3.52	3.36	6.88	3.44
18	3.40	3.31	6.71	3.36
19	3.08	2.96	6.04	3.02
20	3.34	3.21	6.55	3.28
21	3.00	2.86	5.86	2.93
22(10)	2.66	2.92	5.58	2.79
23(16)	3.48	3.35	6.83	3.42
24(19)	3.24	2.92	6.16	3.08

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	47	4.16				
Reps	1	0.03	0.03	2.31		
Lines	23	3.83	0.167	12.85xx	2.01	2.72
Error	23	0.30	0.013			

L.S.D. $t_{.05} = 2.069 \times 0.114 = 0.2359$

$t_{.01} = 2.807 \times 0.114 = 0.3200$

Table 46

Chinese Spring lines with substituted Hope chromosomes.

Chromosome tested	Spike Length Series 1	Series 2	Series 3	Series-4	Total	1953 Average
Hope	10.2	9.7	9.5	9.7	39.1	9.8
Chinese Spring	7.7	7.2	7.3	7.2	29.4	7.4
1	7.8	7.3	7.5	7.5	30.1	7.5
2	6.1	6.3	6.4	6,3	25.1	6.3
3	7.2	7.0	6.8	7.1	28.1	7.0
4	7.7	7.3	7.3	7.7	30.0	7.5
5	7.6	7.6	7.4	7.4	30.0	7.5
6	7.9	7.4	7.5	7.7	30.5	7.6
7	7.0	6.3	6.7	6.6	26.6	6.7
8	8.6	8.6	8.2	8.5	33.9	8.5
9	6.5	6.4	6.1	6.3	25.3	6.3
10	8.7	8.5	8.5	8.4	34.1	8.3
11	7.6	7.3	7.4	7.5	29.8	7.5
12	6.8	7.1	7.0	7.0	27.9	8.0
15	7.7	7.3	7.8	7.1	29.9	7.5
16	7.1	6.9	7.1	7.0	28.1	7.0
17	8.3	8.0	7.9	8.0	32.2	8.0
19	7.9	7.9	7.8	7.6	31-2	7.8
20	9.0	8.4	8.3	9.6	35.3	8.8
21	7.6	7.6	7.3	7.3	29.8	7.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	576.08				
Reps	3	8.53	2.85	6.63		
Lines	19	542.88	28.57	66.44	1.77	2.25
Error	57	24.67	0.43			

L.S.D. 5% point = .46 x 2.002 = 0.92

1% point = .46 x 2.666 = 1.23

Table 47

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Number of Spikelets Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Hope	19.1	19.2	19.1	19.1	76.5	19.1
Chinese Spring	21.5	21.5	21.6	21.5	86.1	21.5
1	22.1	22.2	22.2	22.1	88.6	22.2
2	20.5	20.6	20.5	20.6	82.2	20.6
3	19.6	19.5	19.6	19.6	78.3	19.6
4	21.3	21.5	21.3	21.4	85.5	21.4
5	20.4	20.5	20.4	20.4	81.7	20.4
6	20.0	20.0	20.0	20.0	80.0	20.0
7	18.1	17.9	18.0	18.0	72.0	18.0
8	20.3	20.5	20.4	20.5	81.7	20.4
9	19.6	19.4	19.4	19.5	77.9	20.5
10	19.0	18.9	18.9	18.9	75.7	18.9
11	21.5	21.4	21.6	21.5	86.0	21.5
12	22.3	22.4	22.4	22.3	89.4	22.4
(13)						
15	21.2	21.2	2.3	21.2	84.9	21.2
16	21.1	21.1	21.1	21.1	84.4	21.1
17	21.4	21.3	21.3	21.3	85.3	21.3
(18)						
19	22.3	22.2	22.3	22.3	89.1	22.3
20	20.4	20.4	20.5	20.4	81.7	20.4
21	20.2	20.3	20.2	20.3	81.0	20.3

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	105.58				
Reps	3	0				
Lines	19	105.35	5.54	138.5^{xx}	1.77	2.25
Error	57	0.23	.0040			

L.S.D. 5% point = 0.0444 x 2.002 = 0.09
1% point = 0.0444 x 2.666 = 0.12

Table 48

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Hope	1.87	1.98	2.01	1.97	7.83	1.96
Chinese Spring	2.79	2.99	2.96	2.99	11.73	2.93
1	2.83	3.04	2.96	2.95	11.78	2.95
2	3.36	3.27	3.20	3.27	13.10	3.28
3	2.72	2.79	2.88	2.76	11.15	2.79
4	2.77	2.95	2.92	2.78	11.42	2.86
5	2.68	2.70	2.76	2.76	10.90	2.73
6	2.53	2.70	2.67	2.60	10.50	2.63
7	2.59	2.84	2.69	2.72	10.84	2.71
8	2.36	2.38	2.49	2.41	9.64	2.41
9	3.02	3.03	3.18	3.10	12.33	3.08
10	2.18	2.22	2.22	2.25	8.87	2.22
11	2.83	2.93	2.92	2.87	11.55	2.89
12	3.28	3.15	3.20	3.19	12.82	3.21
15	2.75	2.90	2.73	2.99	11.37	2.84
16	2.97	3.06	2.97	3.01	12.01	3.00
17	2.58	2.66	2.70	2.66	10.60	2.65
19	2.82	2.81	2.86	2.93	11.42	2.86
20	2.27	2.43	2.47	2.13	9.30	2.33
21	2.66	2.67	2.77	2.78	10.88	2.72

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	8.43				
Reps	3	0.09	0.030	6.0		
Lines	19	8.06	0.424	84.8xx	1.77	2.25
Error	57	0.28	0.005			

L.S.D. 5% point = 2.002 x 0.05 = 0.100

1% point = 2.666 x 0.05 = 0.133

Table 49

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Spike Length Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Hope	7.2	7.6	7.3	7.5	29.6	7.40
Chinese Spring	6.7	5.9	6.2	6.1	24.9	6.23
1	6.6	7.2	7.0	7.0	27.8	6.95
2	5.1	5.0	5.3	5.4	20.8	5.20
3	5.7	5.3	5.5	5.9	22.4	5.60
4	6.3	6.5	6.6	6.1	25.5	6.38
5	5.9	6.0	6.1	5.9	23.9	5.98
6	6.8	6.4	6.2	6.0	25.4	6.35
7	4.8	5.4	4.9	5.0	20.1	5.03
8	7.0	7.1	7.5	7.5	29.1	7.28
9	4.7	4.9	5.6	4.7	19.9	4.98
10	6.4	6.8	6.7	6.8	26.7	6.67
11	6.5	6.8	6.4	7.2	26.9	6.73
12	5.8	6.3	6.3	6.0	24.4	6.10
15	6.7	6.0	6.4	6.6	25.7	6.43
16	6.5	6.1	6.0	6.1	24.7	6.18
17	6.7	6.7	6.7	6.8	26.9	6.73
18	6.2	6.2	6.4	5.6	24.4	6.10
19	7.0	6.9	6.8	7.0	27.7	6.93
20	7.1	7.4	7.0	7.2	28.7	7.18
21	5.7	5.7	6.0	5.8	23.2	5.80

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	43.29				
Reps	3	0.06	0.020	0.30		
Lines	20	39.21	1.961	29.27[xx]	1.75	2.20
Error	60	4.02	0.067			

L.S.D. $t_{.05} = 2.000 \times 0.1830 = 0.3660$

$t_{.01} = 2.660 \times 0.1830 = 0.4870$

Table 50

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Number of Spikelets Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Hope	16.9	17.7	16.9	17.4	68.9	17.23
Chinese Spring	22.0	21.0	21.7	21.9	86.6	21.65
1	21.8	23.0	23.4	22.7	90.9	22.73
2	19.3	18.4	20.1	20.3	78.1	19.52
3	18.8	17.2	19.6	19.2	74.8	18.70
4	20.5	21.7	21.6	21.1	84.9	21.23
5	18.6	18.5	20.7	19.4	77.2	19.30
6	20.0	20.3	19.7	19.3	79.3	19.83
7	16.6	17.4	15.7	16.0	65.7	16.43
8	20.8	20.5	21.3	21.0	83.6	20.90
9	18.4	17.9	19.5	18.4	74.2	18.55
10	18.1	18.1	18.7	18.3	73.2	18.30
11	21.6	20.8	22.1	22.0	86.5	21.63
12	21.9	21.2	21.9	21.8	86.8	21.70
13						
14						
15	20.3	20.6	21.9	20.1	82.9	20.73
16	21.6	21.6	21.6	21.1	85.9	21.48
17	21.0	22.2	20.9	21.4	85.5	21.38
18	20.9	20.8	21.3	19.9	82.9	20.73
19	22.2	21.7	21.6	22.9	88.4	22.10
20	21.3	21.6	21.3	22.1	86.3	21.58
21	18.8	18.0	19.9	18.1	74.8	18.70

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	260.44				
Reps	3	3.61	1.203	3.278		
Lines	20	234.79	11.740	31.989^{xx}	1.75	2.20
Error	60	22.04	0.367			

L.S.D. 5% point = 2 x 0.4284 = 0.8568
1% point = 2.66 x 0.4284 = 1.1395

Table 51

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Hope	2.35	2.33	2.32	2.32	9.32	2.33
Chinese Spring	3.29	3.56	3.50	3.60	13.95	3.33
1	3.30	3.19	3.34	3.24	13.07	3.28
2	3.78	3.68	3.79	3.76	15.01	3.75
3	3.30	3.25	3.32	3.25	13.12	3.28
4	3.25	3.33	3.27	3.46	13.31	3.33
5	3.15	3.08	3.39	3.29	12.91	3.23
6	2.94	3.17	3.18	3.22	12.51	3.13
7	3.46	3.22	3.20	3.20	13.08	3.27
8	2.97	2.89	2.84	2.80	11.50	2.88
9	3.91	3.25	3.48	3.91	14.55	3.64
10	2.83	2.66	2.79	2.69	10.97	2.74
11	3.32	3.06	3.25	3.06	12.69	3.17
12	3.78	3.36	3.47	3.63	14.24	3.56
15	3.03	3.43	3.42	3.04	12.92	3.23
16	3.32	3.54	3.60	3.46	13.92	3.48
17	3.14	3.31	3.12	3.14	12.71	3.18
18	3.37	3.35	3.33	3.55	13.60	3.40
19	3.17	3.14	3.18	3.27	12.76	3.19
20	3.00	2.92	3.04	3.07	12.03	3.01
21	3.30	3.16	3.32	3.12	12.90	3.23

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	8.93				
Reps	3	0.05	0.017	1.0		
Lines	20	7.85	0.393	23.118xx	1.75	2.20
Error	60	1.03	0.017			

L.S.D. 5% point = 2.00 x 0.0922 = 0.184

1% point = 2.66 x 0.0922 = 0.245

Table 52

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Spike Length Series 1	Series 2	Series 3	Series 4	Total A	1953 Average
Timstein	7.1	7.5	7.2	7.2	29.0	7.3
Chinese Spring	7.5	7.7	7.8	7.6	30.6	7.7
1	7.6	7.6	7.4	7.7	30.3	7.6
2	7.0	6.9	7.2	7.1	28.2	7.1
3	8.4	8.6	8.3	8.5	33.8	8.5
4	7.3	7.5	7.4	7.2	29.4	7.4
5	7.4	7.4	7.2	7.3	29.3	7.4
6	7.6	7.8	7.5	7.7	30.6	7.7
7	7.1	7.4	7.3	7.4	29.2	7.3
8	7.7	7.9	7.7	7.8	31.1	7.8
9	7.0	7.4	7.4	7.1	28.9	7.2
10	8.1	8.0	7.8	7.8	31.7	7.9
11	8.4	8.8	8.6	8.6	34.4	8.6
12	6.6	6.3	6.4	6.5	25.8	6.5
15	7.2	7.3	6.9	7.0	28.4	7.1
16	7.7	7.9	7.6	7.7	30.9	7.7
17	7.9	7.9	8.3	8.1	32.2	8.1
18	7.6	7.6	7.3	7.3	29.8	7.5
19	7.6	8.0	8.0	7.9	31.5	7.9
20	9.8	9.6	9.2	9.3	37.9	9.5
21	8.1	8.0	7.7	7.9	31.7	7.9

Analysis of Variance

Source	df	ss	Ms	F	5%	1%
Total	83	337.98				
Reps	3	2.43	0.81	3.51		
Lines	20	322.00	16.10	70.00^{xx}	1.75	2.20
Error	60	13.55	0.23			

L.S.D. 5% point = .34 x 2.00 = 0.68

1% point = .34 x 2.66 = 0.90

Table 53

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Number of Spikelets Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Timstein	13.2	13.0	12.5	12.4	51.1	12.8
Chinese Spring	22.4	22.5	21.8	22.3	89.0	22.3
1	21.4	20.6	21.9	21.6	85.5	21.4
2	20.5	21.3	20.9	20.9	83.6	20.9
3	20.6	21.6	21.9	21.9	86.0	21.5
4	21.3	21.9	21.9	22.0	87.1	21.8
5	19.5	19.4	19.5	19.6	78.0	19.5
6	20.2	20.0	20.3	20.3	80.8	20.2
7	19.8	19.4	19.6	19.6	78.4	19.6
8	20.6	20.2	20.4	20.4	81.6	20.4
9	20.3	20.5	20.7	20.5	82.0	20.5
10	21.7	21.6	21.8	21.6	86.7	21.7
11	22.5	22.8	22.9	23.0	91.2	22.8
12	20.4	20.6	20.5	20.5	82.0	20.5
15	21.6	21.8	21.9	21.8	87.1	21.8
16	20.8	20.8	20.8	20.8	83.2	20.8
17	22.2	22.1	22.2	22.1	88.6	22.2
18	21.8	21.9	21.9	21.7	87.3	21.8
19	21.3	21.2	21.3	21.3	85.1	21.3
20	20.8	20.8	20.7	20.8	83.1	20.8
21	21.5	21.6	21.6	21.5	86.2	21.6

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	329.87				
Reps	3	0.19	0.063			
Lines	20	325.82	16.29	254.5xx	1.75	2.20
Error	60	3.86	.064			

L.S.D. 5% point = .18 x 2.00 = 0.36

1% point = .18 x 2.66 = 0.48

Table 54

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Timstein	1.86	1.73	1.74	1.72	7.05	1.76
Chinese Spring	2.99	2.92	2.79	2.93	11.63	2.91
1	2.81	2.71	2.96	2.81	11.29	2.82
2	2.93	3.07	2.90	2.94	11.84	2.96
3	2.45	2.51	2.64	2.58	10.18	2.54
4	2.92	2.92	2.96	3.06	11.86	2.97
5	2.64	2.62	2.71	2.68	10.65	2.66
6	2.66	2.56	2.71	2.64	10.57	2.64
7	2.79	2.62	2.68	2.65	10.74	2.69
8	2.68	2.56	2.65	2.62	10.51	2.63
9	2.90	2.77	2.80	2.89	11.36	2.84
10	2.68	2.70	2.79	2.77	10.94	2.74
11	2.68	2.59	2.66	2.67	10.60	2.65
12	3.09	3.27	3.20	3.15	12.71	3.18
15	3.00	2.99	3.17	3.11	12.27	3.07
16	2.70	2.63	2.74	2.70	10.77	2.69
17	2.81	2.80	2.67	2.73	11.01	2.75
18	2.86	2.88	3.00	2.97	11.71	2.93
19	2.80	2.65	2.66	2.70	10.81	2.70
20	2.12	2.17	2.25	2.24	8.78	2.19
21	2.65	2.70	2.81	2.72	10.88	2.72

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	7.50				
Reps	3	0.4	0.133	31.9^{xx}	2.76	4.13
Lines	20	7.21	0.361	86.0^{xx}	1.75	2.20
Error	60	0.25	0.0042			

L.S.D. $t_{.05} = 2.000 \times 0.046 = 0.092$

$t_{.01} = 2.660 \times 0.046 = 0.1223$

Table 55

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Spike Length Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Timstein	5.6	6.0	6.0	6.0	23.6	5.90
Chinese Spring	6.4	6.1	6.4	6.6	25.5	6.38
1	6.8	6.5	6.3	6.5	26.1	6.53
2	5.6	5.4	5.8	6.3	23.1	5.78
3	7.1	6.8	7.0	6.8	27.7	6.93
4	5.6	5.7	5.7	6.2	23.2	5.80
5	6.3	5.9	6.2	6.4	24.8	6.20
6	6.0	5.9	6.5	6.3	24.7	6.18
7	5.7	5.8	5.9	6.0	23.4	5.85
8	6.2	6.4	6.4	6.0	25.0	6.25
9	5.3	5.5	5.6	5.6	22.0	5.50
10	6.8	6.7	6.7	7.0	27.2	6.80
11	7.0	7.0	7.4	7.3	28.7	7.18
12	5.4	5.0	5.6	5.6	21.6	5.40
15	6.5	6.5	6.3	6.7	26.0	6.50
16	6.5	6.5	6.6	6.6	26.2	6.55
17	6.3	6.4	6.2	6.6	25.5	6.38
18	6.2	6.0	6.3	6.1	24.6	6.15
19	6.7	6.6	6.8	7.1	27.2	6.80
20	7.8	7.6	8.0	7.9	31.3	7.83
21	6.8	6.5	6.6	6.7	26.6	6.65

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	28.88				
Reps	3	0.79	0.263	8.22		
Lines	20	26.26	1.313	41.03xx	1.75	2.20
Error	60	1.94	0.032			

L.S.D. 5% point = .126 x 2.00 = .252

1% point = .126 x 2.66 = .435

Table 56

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Number of Spikelets Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Timstein	11.9	12.5	11.9	12.0	48.3	12.08
Chinese Spring	22.1	21.5	22.0	22.0	87.6	21.90
1	21.8	21.9	20.7	21.8	86.2	21.55
2	20.3	19.7	22.5	21.1	83.6	20.90
3	21.3	20.9	22.1	19.8	84.1	21.03
4	20.0	21.1	20.7	22.3	84.1	21.03
5	19.4	19.9	19.6	19.8	78.7	19.68
6	19.1	19.1	20.8	20.6	79.6	19.90
7	19.3	19.5	19.3	19.5	77.6	19.40
8	19.3	20.5	20.7	20.1	80.6	20.15
9	19.8	20.3	20.1	20.1	80.3	20.08
10	20.7	20.7	21.3	21.3	84.0	21.00
11	22.1	21.4	21.9	22.2	87.6	21.90
12	20.3	19.3	20.5	19.3	79.4	19.85
15	22.2	22.3	21.7	21.3	87.5	21.88
16	21.3	21.1	21.3	21.7	85.4	21.35
17	21.8	21.3	21.5	21.9	86.5	21.63
18	21.5	21.6	22.5	20.8	86.4	21.60
19	21.1	20.6	21.6	22.3	85.6	21.40
20	21.1	21.2	21.9	21.1	85.3	21.33
21	21.8	20.8	21.3	22.2	86.3	21.53

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	373.26				
Reps	3	2.44	0.813	2.377		
Lines	20	350.21	17.511	51.202^{xx}	1.75	2.20
Error	60	20.51	0.342			

L.S.D. 5% point = 2.00 x 0.414 = 0.828

1% point = 2.66 x 0.414 = 1.101

Table 57

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Spike Density Series 1	Series 2	Series 3	Series 4	Total	1954 Average
Timstein	2.13	2.08	1.98	2.00	8.19	2.05
Chinese Spring	3.45	3.52	3.44	3.33	13.74	3.44
1	3.20	3.37	3.29	3.35	13.21	3.30
2	3.63	3.65	3.88	3.35	14.51	3.63
3	3.00	3.07	3.16	2.91	12.14	3.04
4	3.57	3.70	3.63	3.60	14.50	3.63
5	3.08	3.37	3.16	3.09	12.70	3.18
6	3.18	3.24	3.20	3.27	12.89	3.22
7	3.39	3.36	3.27	3.10	13.12	3.28
8	3.11	3.20	3.23	3.35	12.89	3.22
9	3.74	3.69	3.59	3.59	14.61	3.65
10	3.04	3.09	3.18	3.04	12.35	3.09
11	3.16	3.06	2.96	3.04	12.22	3.06
12	3.76	3.86	3.66	3.45	14.73	3.68
15	3.42	3.43	3.44	3.18	13.47	3.37
16	3.28	3.25	3.38	3.29	13.20	3.30
17	3.46	3.33	3.46	3.32	13.57	3.39
18	3.47	3.60	3.57	3.41	14.05	3.51
19	3.15	3.12	3.18	3.14	12.59	3.15
20	2.71	2.79	2.74	2.80	11.04	2.76
21	3.21	3.20	3.22	3.31	12.94	3.24

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	83	10.99				
Reps	3	0.12	0.040	4.7^{xx}	2.76	4.13
Lines	20	10.36	0.518	60.94^{xx}	1.75	2.20
Error	60	0.51	0.0085			

L.S.D. 5% point = 2.00 x 0.0652 = 0.1304

1% point = 2.66 x 0.0652 = 0.1734

Table 58

Computation of lines x years interaction from composite of 3 sets of substitution lines in 1953 and 1954

Chromosome tested	Thatcher 1953 Rep 1	Rep 2	Rep 3	Rep 4	1954 Rep 1	Rep 2	Rep 3	Rep 4	Hope 1953 Rep 1	Rep 2	Rep 3	Rep 4	1954 Rep 1	Rep 2	Rep 3	Rep 4	Timstein 1953 Rep 1	Rep 2	Rep 3	Rep 4	1954 Rep 1	Rep 2	Rep 3	Rep 4
Chinese Spring	560	520	550	560	290	360	350	360	590	650	640	530	380	365	390	385	630	575	600	630	350	355	345	310
1	1020	1060	970	1020	500	535	460	730	840	950	830	880	450	485	550	620	980	950	935	875	500	590	560	530
2	810	760	750	790	470	460	410	630	550	650	670	640	330	480	500	510	700	560	670	550	500	540	460	430
3	750	770	800	690	520	370	470	640	600	700	620	660	345	450	340	630	710	610	670	680	450	530	380	420
4	620	550	570	610	285	240	275	290	670	650	680	650	430	515	490	550	820	750	800	740	490	530	425	500
5	900	780	740	750	440	450	525	640	740	700	700	800	425	460	520	510	650	730	620	590	425	470	460	520
6	640	560	570	530	600	400	430	650	800	760	750	680	450	420	495	635	640	630	700	665	335	530	555	450
7	750	720	720	710	420	480	530	520	830	860	780	760	510	460	560	590	640	520	740	580	500	430	500	490
8	800	930	810	900	490	530	500	600	810	740	730	800	400	480	450	710	850	850	810	960	480	610	580	440
9	760	760	810	780	490	410	420	550	750	740	830	680	415	490	530	570	580	545	520	600	530	480	450	325
10	680	680	720	650	460	520	420	430	750	710	750	700	390	530	550	580	435	470	320	490	400	340	540	430
11	560	560	480	490	210	325	265	300	520	520	600	570	320	370	325	410	580	630	650	615	380	450	425	400
12	720	720	740	750	470	570	400	550	900	840	930	840	535	520	540	600	570	650	700	725	460	460	470	420
15	530	500	450	650	435	310	410	465	550	640	650	660	440	485	430	550	640	600	770	460	310	320	360	490
16	580	620	530	540	400	420	330	425	570	490	570	640	330	385	380	410	570	750	730	710	335	480	540	620
19	640	700	660	600	520	425	485	550	430	630	680	760	420	380	435	430	750	830	960	720	535	520	490	565
20	640	580	570	610	375	530	415	460	600	610	600	600	330	420	405	415	615	630	620	660	420	390	450	420
21	700	680	820	710	425	390	550	530	730	780	850	750	430	470	580	565	710	720	660	615	435	310	450	505

Table 58 (continued)

Analysis of Variance

Source of Variance	df	ss	ms	F	5%	1%
Reps	3	86866.0	28955.3			
Years	1	5678752.1	5678752.1			
Varieties	2	27067.8	13533.9			
YxV	2	9005.6	4502.8			
Error (1)	15	220780.5	14718.7			
Lines	17	2003724.8	117866.2			
LxY	17	34033.1	2001.9	0.07	1.93	2.55
LxV	34	1037489.7	30514.4	6.05^{x}	1.47	1.72
LxYxV	34	59491.7	1749.8	0.35	1.47	1.72
Error (2)	306	1543088.5	5042.8			

		LxYxV	LxV	L
L.S.D.	5% level	98.9	98.9	144.9
	1% level	130.0	130.0	194.6

Table 59

Computation of lines x varieties interaction of yield from composite of 3 sets of substitution lines in 1953.

Chromosome tested	Thatcher (1)				Ave.	Hope				Ave.	Timstein				Ave.
Chinese Spring	560	520	550	560	547.5	590	650	640	530	602.5	630	575	600	630	608.75
1	1020	1060	970	1020	1017.5	840	950	830	880	875.0	980	950	935	875	935.0
2	810	760	750	790	777.5	550	650	670	640	627.5	700	560	670	550	620.0
3	750	770	800	690	752.5	600	700	620	660	645.0	710	610	670	680	667.5
4	620	550	570	610	587.5	670	650	680	650	662.5	820	750	800	740	777.5
5	900	780	740	750	792.5	740	700	700	800	735.0	650	730	620	590	647.5
6	640	560	570	530	575.0	800	760	750	680	747.5	640	630	700	665	658.75
7	750	720	720	710	725.0	830	860	780	760	807.5	640	520	740	580	620.0
8	800	930	810	900	860.0	810	740	730	800	770.0	850	850	810	960	867.5
9	760	760	810	780	777.5	750	740	830	680	750.0	580	545	520	600	561.25
10	680	680	720	650	682.5	750	710	750	700	727.5	435	470	320	490	428.75
11	560	560	480	490	522.5	520	520	600	570	552.5	580	630	650	615	618.75
12	720	720	740	750	732.5	900	840	930	840	877.5	570	650	700	725	661.25
15	530	500	450	650	532.5	550	640	650	660	625.0	640	600	770	460	617.5
16	580	620	530	540	567.5	570	490	570	640	567.5	570	750	730	710	690.0
19	640	700	660	600	650.0	430	630	680	760	625.0	750	830	960	720	815.0
20	640	580	570	610	600.0	600	610	600	600	602.5	615	630	620	660	631.25
21	700	680	820	710	727.5	730	780	850	750	777.5	710	720	660	615	676.25

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	215					
Reps	3	6524	2175.0			
Varieties	2	26203	13102.0			
Error (1)	6	21247	3541.0			
Lines	17	1777660	104568.0			
Lines x varieties	34	986639	29019	9.07xx	1.51	1.78
Error (2)	153	489554	3200			

L.S.D.	5% level	79.1
	1% level	104.6

Table 60

Computation of lines x varieties interaction from composite of 3 sets of substitution lines in 1954.

Chromosome tested	Thatcher set of substitution lines						Ave.	Hope set of substitution lines						Ave.	Timstein set of substitution lines						Ave.
Thatcher	810	890	825	830	850	790	832.5	810	770	830	830	780	810	805.0	805	840	900	810	845	790	831.7
Timstein	920	665	770	930	900	850	839.2	875	760	850	880	830	870	844.2	805	640	770	910	950	895	828.3
Chinese Sp.	290	360	350	360	400	380	356.7	380	3.65	390	385	350	330	366.7	350	355	345	310	380	410	358.3
1	500	535	460	730	630	540	565.8	450	485	550	620	550	580	539.2	500	590	560	530	510	550	540.0
2	470	460	410	630	585	400	492.5	330	480	500	510	560	480	476.7	500	540	460	430	490	380	466.7
3	520	370	470	640	465	600	510.8	345	450	340	630	640	515	486.7	450	530	380	420	360	515	442.5
4	285	240	275	290	225	240	259.2	430	515	490	550	550	450	497.5	490	530	425	500	530	460	489.2
5	440	450	525	640	460	490	500.8	425	460	520	510	550	530	499.2	425	470	460	520	450	410	455.8
6	600	400	430	650	540	475	515.8	450	420	495	635	550	515	510.8	335	530	555	450	585	360	469.2
7	420	480	530	520	500	500	491.7	510	460	560	590	610	400	521.7	500	430	500	490	495	460	479.2
8	490	530	500	600	510	500	521.7	400	480	450	710	410	585	505.8	480	610	580	440	640	480	538.3
9	490	410	420	550	500	400	461.7	415	490	530	570	490	515	501.7	430	480	450	325	390	360	405.8
10	460	520	420	430	410	485	454.2	390	530	550	580	530	525	517.5	400	340	540	430	410	410	421.7
11	210	325	265	300	370	220	281.7	320	370	325	410	540	265	371.7	380	450	425	400	340	360	392.5
12	470	570	400	550	450	450	481.7	535	520	540	600	500	575	545.0	460	460	470	420	410	430	458.3
15	435	310	410	465	480	320	403.3	440	485	430	550	450	445	466.7	310	320	360	490	335	325	356.7
16	400	420	330	425	430	440	407.5	330	385	380	410	340	430	379.2	335	480	540	620	470	400	474.2
18	190	175	250	200	210	150	195.8	425	445	440	465	490	405	445.0	405	365	550	550	460	465	465.8
19	520	425	485	550	515	420	485.8	420	380	435	430	400	510	429.2	535	520	490	565	500	520	521.7
20	375	530	415	460	510	305	432.5	330	420	405	415	450	410	405.0	420	390	450	420	430	470	430.0
21	425	390	550	530	600	560	509.2	430	470	580	565	605	555	534.2	435	310	450	505	535	580	469.2

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	377					
Reps	3	243359	81119.7			
Varieties	2	60210	30105.0			
Error (1)	6	85612	14268.7			
Lines	20	5605071	2802536			
Lines x varieties	40	706998	17674.9	5.06^{xx}	1.43	1.66
Error (2)	306	1068588	3492.1			

L.S.D. 5% level = 67.8
1% level = 89.1

Table 61

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Series 1	Series 2	Series 3	Series 4	1952 Total	Average
	Yield in Grams					
Thatcher	955	1020	1040	1000	4015	1003.75
Chinese Spring	661	612	740	655	2668	667.00
1	840	1000	900	895	3635	908.75
2	785	855	708	755	3103	775.75
3	840	800	885	880	3405	851.25
4	724	535	835	545	2639	659.75
5	846	795	763	562	2966	741.50
6	883	870	805	655	3213	803.25
7	631	813	487	762	2693	673.25
8	942	1008	840	845	3635	908.75
9	864	670	860	735	3129	782.25
10	934	620	600	807	2961	740.25
11	686	780	588	644	2698	674.50
12	782	1000	925	1092	3799	949.75
15	791	773	820	842	3226	806.50
16	463	320	634	360	1777	444.25
17	615	708	632	862	2817	704.25
19	812	1055	665	695	3227	806.75
20	712	740	762	740	2954	738.50
21	766	825	836	890	3317	829.25

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	1819960				
Reps	3	9756	3252	0.292		
Lines	19	1174666	61815	5.54^{xx}	1.72	2.15
Error	57	635538	11150			

L.S.D. - 5% point - 149.35

1% point - 198.88

Table 62

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Yield in Grams Series 1	Series 2	Series 3	Series 4	1953 Total	Average
Thatcher	1200	1210	1250	1160	4820	1205
Chinese Spring	560	520	550	560	2190	547.5
1	1020	1060	970	1020	4070	1017.5
2	810	760	750	790	3110	777.5
3	750	770	800	690	3010	752.5
4	620	550	570	610	2350	587.5
5	900	780	740	750	3170	792.5
6	640	560	570	530	2300	575.0
7	750	720	720	710	2900	725.0
8	800	930	810	900	3440	860.0
9	760	760	810	780	3110	777.5
10	680	680	720	650	2730	682.5
11	560	560	480	490	2090	522.5
12	720	720	740	750	2930	732.5
13	570	590	600	540	2300	575.0
15	530	500	450	650	2130	532.5
16	580	620	530	540	2270	567.5
17	380	510	460	400	1750	437.5
18	480	600	570	630	2280	570.0
19	640	700	660	600	2600	650.0
20	640	580	570	610	2400	600.0
21	700	680	820	710	2910	727.5

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	87	2734177.3				
Reps	3	2422.3	807.433	0.370		
Lines	21	2594127.3	123529.871	56.547^{xx}	1.73	2.17
Error	63	13762.77	2184.567			

L.S.D. $t_{.05}$ 1.999 x 33.05 = 66.07

$t_{.01}$ 2.657 x 33.05 = 87.81

Table 63

Chinese Spring lines with substituted Thatcher chromosomes

Chromosome tested	Yield in Grams Series 1	Series 2	Series 3	Series 4	Series 5	Series 6	1954 Total	Average
1	500	535	460	730	630	540	3395	565.8
2	470	460	410	630	585	400	2955	492.5
3	520	370	470	640	465	600	3065	510.8
4	285	240	275	290	225	240	1555	259.2
5	440	450	525	640	460	490	3005	500.8
6	600	400	430	650	540	475	3095	515.8
7	420	480	530	520	500	500	2950	491.7
8	490	530	500	600	510	500	3130	521.7
9	490	410	420	550	500	400	2770	461.7
10	460	520	420	430	410	485	2725	454.2
11	210	325	265	300	370	220	1690	281.7
12	470	570	400	550	450	450	2890	481.7
13	290	260	310	335	250	220	1665	277.5
15	435	310	410	465	480	320	2420	403.3
16	400	420	330	425	430	440	2445	407.5
18	190	175	250	200	210	150	1175	195.8
19	520	425	485	550	515	420	2915	485.8
20	375	530	415	460	510	305	2595	432.5
21	425	390	550	530	600	560	3055	509.2
22(10)	550	465	410	400	490	410	2725	454.2
23(16)	450	395	420	415	460	385	2525	420.8
24(19)	480	530	400	550	440	430	2830	471.7
Thatcher	810	890	825	830	850	790	4995	832.5
Chinese Spring	290	360	350	360	400	380	2140	356.7
Timstein	920	665	770	930	900	850	5035	839.2

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	3569725				
Reps	5	129157				
Lines	24	3025570	126065.4	36.5		
Error	120	414998	3458.3			

L.S.D. - 5% point 1.982 x 34 = 67.39

1% point 2.261 x 34 = 89.11

Table 64

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Yield in Grams Series 1	Series 2	Series 3	Series 4	1953 Total	Average
Hope						
Chinese Spring	590	650	640	530	2410	602.5
1	840	950	830	880	3500	875.0
2	550	650	670	640	2510	627.5
3	600	700	620	660	2580	645.0
4	670	650	680	650	2650	662.5
5	740	700	700	800	2940	735.0
6	800	760	750	680	2990	747.5
7	830	860	780	760	3230	807.5
8	810	740	730	800	3080	770.0
9	750	740	830	680	3000	750.0
10	750	710	750	700	2910	727.5
11	520	520	600	570	2210	552.5
12	900	840	930	840	3510	877.5
15	550	640	650	660	2500	625.0
16	570	490	570	640	2270	567.5
17	560	630	600	720	2510	627.5
* 19	430	630	680	760	2500	625.0
20	600	610	600	600	2410	602.5
21	730	780	850	750	3110	777.5

* poor germination, not included in analysis.

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	71	804711				
Reps	3	5022	1674	0.72	2.79	4.19
Lines	17	680811	40048	17.10^{xx}	1.83	2.34
Error	51	118878	2331			

L.S.D. - 5% point = 67.870

1% point = 90.584

Table 65

Chinese Spring lines with substituted Hope chromosomes

Chromosome tested	Yield in Grams Series 1	Series 2	Series 3	Series 4	Series 5	1954 Series 6	Total	Average
1	450	485	550	620	550	580	3235	539.2
2	330	480	500	510	560	480	2860	476.7
3	345	450	340	630	640	515	2920	486.7
4	430	515	490	550	550	450	2985	497.5
5	425	460	520	510	550	530	2995	499.2
6	450	420	495	635	550	515	3065	510.8
7	510	460	560	590	610	400	3130	521.7
8	400	480	450	710	410	585	3035	505.8
9	415	490	530	570	490	515	3010	501.7
10	390	530	550	580	530	525	3105	517.5
11	320	370	325	410	540	265	2230	371.7
12	535	520	540	600	500	575	3270	545.0
15	440	485	430	550	450	445	2800	466.7
16	330	385	380	410	340	430	2275	379.2
17	470	460	470	420	550	435	2805	467.5
18	425	445	440	465	490	405	2670	445.0
19	420	380	435	430	400	510	2575	429.2
20	330	420	405	415	450	410	2430	405.0
21	430	470	580	565	605	555	3205	534.2
Hope	640	640	635	710	730	700	4055	675.8
Chinese Spring	380	365	390	385	350	330	2200	366.7
Regent	630	755	785	620	840	815	4445	740.8
Thatcher	810	770	830	830	780	810	4830	805.0
Timstein	875	760	850	880	830	870	5065	844.2
Red Bobs	370	460	560	565	500	545	3000	500.0

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	2734222				
Reps	5	176418	35284.0			
Lines	24	2181118	90879.9	28.9		
Error	120	377686	3147.4			

L.S.D. - 5% point = 32.4 x 1.982 = 64.42

1% point = 32.4 x 2.621 = 84.92

Table 66

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Yield in Grams Series 1	Series 2	Series 3	Series 4	Total	1953 Average
Timstein	1110	1030	1080	1130	4350	1087.50
Chinese Spring	630	575	600	630	2435	608.75
1	980	950	935	875	3740	935.00
2	700	560	670	550	2480	620.00
3	710	610	670	680	2670	667.50
4	820	750	800	740	3110	777.50
5	650	730	620	590	2590	647.50
6	640	630	700	665	2635	658.75
7	640	520	740	580	2480	620.00
8	850	850	810	960	3470	867.50
9	580	545	520	600	2245	561.25
* 10	435	470	320	490	1715	428.75
11	580	630	650	615	2475	618.75
12	570	650	700	725	2645	661.25
15	640	600	770	460	2470	617.50
16	570	750	730	710	2760	690.00
17	660	540	740	630	2570	642.50
18	580	650	700	620	2550	637.50
19	750	830	960	720	3260	815.00
20	615	630	620	660	2525	631.25
21	710	720	660	615	2705	676.25

* poorer stand because of low germination therefore not included in analysis.

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	79	1569420				
Reps	3	27640	9213.3	1.04	2.77	4.14
Lines	19	1037420	54601.0	6.07xx	1.72	2.15
Error	57	504360	8848.4			

L.S.D. - 5% point = 133.133

1% point = 177.289

Table 67

Chinese Spring lines with substituted Timstein chromosomes

Chromosome tested	Series 1	Series 2	Series 3	Series 4	Series 5	Series 6	1954 Total	Average
			Yield in Grams					
1	500	590	560	530	510	550	3240	540.00
2	500	540	460	430	490	380	2800	466.67
3	450	530	380	420	360	515	2655	442.50
4	490	530	425	500	530	460	2935	489.16
5	425	470	460	520	450	410	2735	455.83
6	335	530	555	450	585	360	2815	469.17
7	500	430	500	490	495	460	2875	479.17
8	480	610	580	440	640	480	3230	538.33
9	430	480	450	325	390	360	2435	405.83
10	400	340	540	430	410	410	2530	421.67
11	380	450	425	400	340	360	2355	392.50
12	460	460	470	420	510	430	2750	458.33
15	310	320	360	490	335	325	2140	356.67
16	335	480	540	620	470	400	2845	474.17
17	435	420	550	440	450	395	2690	448.33
18	405	365	550	550	460	465	2795	465.83
19	535	520	490	565	500	520	3130	521.67
20	420	390	450	420	430	470	2580	430.00
21	435	310	450	505	535	580	2815	469.17
Timstein	805	640	770	910	950	895	4970	828.33
Chinese Spring	350	355	345	310	380	410	2150	358.33
Regent	700	800	710	670	660	825	4365	727.50
Thatcher	805	840	900	810	845	790	4990	831.67
Reward	450	510	600	600	660	635	3455	575.83
Red Bobs	440	440	515	460	550	520	2925	487.50

Analysis of Variance

Source	df	ss	ms	F	5%	1%
Total	149	2723795				
Reps	5	42705	85.41			
Lines	24	2196574	91523.9	26.6xx		
Error	120	484516	4037.6			

L.S.D. - 5% point = 1.982 x 36.7 = 72.74

1% point = 2.621 x 36.7 = 96.19